

78225

## RECEIVED SEARCH REQUEST FORM

Access DB# \_\_\_\_\_

OCT 21 2002 Scientific and Technical Information Center

Requester's Full Name: John Lin Examiner #: 6957 Date: 10-21-02  
 Art Unit: 1646 Phone Number 303-4008 Serial Number: 09/838028  
 Mail Box and Bldg/Room Location: CM1 10D19 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.  
 \*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_  
 Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEO IP NO! 2 of  
 09/838028. (two)

10D19

Point of Contact:  
 Beverly Shears  
 Technical Info. Specialist  
 CM1 1E05 Tel: 308-4994

## STAFF USE ONLY

## Type of Search

## Vendors and cost where applicable

Searcher: Beverly 4994 NA Sequence (#) \_\_\_\_\_ STN \_\_\_\_\_  
 Searcher Phone #: \_\_\_\_\_ AA Sequence (#) \_\_\_\_\_ Dialog \_\_\_\_\_  
 Searcher Location: \_\_\_\_\_ Structure (#) \_\_\_\_\_ Questel/Orbit \_\_\_\_\_  
 Date Searcher Picked Up: \_\_\_\_\_ Bibliographic \_\_\_\_\_ Dr. Link \_\_\_\_\_  
 Date Completed: 10-22-02 Litigation \_\_\_\_\_ Lexis/Nexis \_\_\_\_\_  
 Searcher Prep & Review Time: 3 Fulltext \_\_\_\_\_ Sequence Systems \_\_\_\_\_  
 Clerical Prep Time: \_\_\_\_\_ Patent Family \_\_\_\_\_ WWW/Internet \_\_\_\_\_  
 Online Time: 20 Other \_\_\_\_\_ Other (specify) CGN

**THIS PAGE BLANK (USPTO)**

Tue Oct 22 10:58:57 2002

us-09-838-028-2.rapm

Ulm  
09/838028 Page 1  
Seq. ID 2 w/Interf

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2002, 16:08:45 : Search time 113 Seconds  
(without alignments)  
1404.807 Million cell updates/sec

Title: US-09-838-028-2  
2318  
Sequence: 1 MESSPIRQSGNSSTLGRVP.....SDIIMSDSYLRPASPRLS 451

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues  
Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending-Patents\_AA\_Main: \*  
1: /cgn2\_6/ptodata/1/paa/PCRTUS\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep: \*  
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25: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep: \*  
26: /cgn2\_6/ptodata/1/paa/US103\_COMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2318	100.0	451	1 PCT-US01-10436-3	Sequence 3, Appli
2	2318	100.0	451	19 US-09-533-687-2	Sequence 12, Appli
3	2318	100.0	451	21 US-09-714-008A-12	Sequence 2, Appli
4	2318	100.0	451	21 US-09-740-0033-2	Sequence 2, Appli
5	2318	100.0	451	22 US-09-815-499-2	Sequence 2, Appli
6	2318	100.0	451	22 US-09-838-028-2	Sequence 2, Appli
7	2318	100.0	451	22 US-09-860-797-2	Sequence 2, Appli

8	2318	100.0	451	22	US-09-864-029-22	Sequence 22, Appli
9	2318	100.0	451	23	US-09-980-049-3	Sequence 3, Appli
10	2318	100.0	451	23	US-09-995-543-12	Sequence 12, Appli
11	2318	100.0	451	24	US-10-096-511-12	Sequence 12, Appli
12	2318	100.0	451	26	US-60-202-278-1	Sequence 1, Appli
13	2318	100.0	451	26	US-60-317-661-2	Sequence 2, Appli
14	2318	100.0	451	26	US-60-329-926-2	Sequence 2, Appli
15	2318	100.0	869	21	US-09-714-008A-100	Sequence 100, App
16	2318	100.0	869	23	US-09-995-543-100	Sequence 100, App
17	2318	100.0	869	24	US-10-096-511-100	Sequence 100, App
18	2317	100.0	451	22	US-09-864-029-24	Sequence 24, Appli
19	2313	99.8	451	21	US-09-714-008A-84	Sequence 84, Appli
20	2313	99.8	451	23	US-09-995-543-84	Sequence 84, Appli
21	2313	99.8	451	24	US-10-096-511-84	Sequence 84, Appli
22	2219	95.7	529	26	US-60-212-655-705	Sequence 705, App
23	2219	95.7	529	26	US-60-229-515-939	Sequence 939, App
24	2219	95.7	555	26	US-60-212-655-407	Sequence 407, App
25	2219	95.7	555	26	US-60-229-515-974	Sequence 974, App
26	2219	95.7	672	26	US-60-329-515-1243	Sequence 1243, Ap
27	2204	95.1	449	22	US-09-838-028-4	Sequence 4, Appli
28	2106	90.9	417	26	US-60-317-661-11	Sequence 11, Appli
29	2106	90.9	417	26	US-60-329-926-11	Sequence 11, Appli
30	1276	55.0	252	9	US-08-513-974-52	Sequence 52, Appli
31	1276	55.0	252	18	US-09-461-436-52	Sequence 360, Appli
32	1276	55.0	252	18	US-09-461-436-360	Sequence 1253, Ap
33	1276	55.0	252	22	US-09-864-029-36	Sequence 263, App
34	1162	50.1	221	26	US-60-192-587-1253	Sequence 1254, Ap
35	999.5	43.1	196	26	US-60-186-281-263	Sequence 221, App
36	999.5	43.1	201	26	US-60-192-738-306	Sequence 306, App
37	999.5	43.1	201	26	US-60-194-114-221	Sequence 221, App
38	992	42.8	187	26	US-60-192-587-1254	Sequence 1254, Ap
39	887	38.3	169	26	US-60-196-713-2476	Sequence 2476, Ap
40	823	35.5	422	22	US-09-864-029-37	Sequence 37, Appli
41	823	35.5	428	26	US-60-317-661-12	Sequence 12, Appli
42	823	35.5	428	26	US-60-329-926-12	Sequence 12, Appli
43	821.5	35.4	419	21	US-09-740-0033-4	Sequence 4, Appli
44	790.5	34.1	160	26	US-60-192-587-1124	Sequence 1124, Ap
45	790.5	34.1	160	26	US-60-194-091-1107	Sequence 1107, Ap

#### ALIGNMENTS

RESULT 1  
PCT-US01-10436-3  
: Sequence 3, Application PCT/US0110436  
: GENERAL INFORMATION:  
: APPLICANT: INCYTE GENOMICS, INC.  
: APPLICANT: POLICKY, Jennifer L.  
: APPLICANT: TRIBOULEY, Catherine M.  
: APPLICANT: TANG, Y. Tom  
: APPLICANT: BAUGHN, Mariah R.  
: APPLICANT: GRAUL, Richard  
: APPLICANT: KHAN, Farrah A.  
: APPLICANT: NGUYEN, Daniel B.  
: APPLICANT: PATTERSON, Chandra  
: APPLICANT: LAL, Preeti  
: APPLICANT: AU-YOUNG, Janice  
: APPLICANT: YANG, Junming  
: APPLICANT: HAFALIA, April  
: APPLICANT: WALIA, Narinder K.  
: APPLICANT: DAS, Debopriya  
: TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS  
: FILE REFERENCE: PI-0072 PCT  
: CURRENT APPLICATION NUMBER: PCT/US01/10436  
: PRIOR FILING DATE: 2001-03-29  
: PRIOR APPLICATION NUMBER: 60/193,051  
: PRIOR FILING DATE: 2000-03-29  
: PRIOR APPLICATION NUMBER: 60/195,155  
: PRIOR FILING DATE: 2000-04-06  
: PRIOR APPLICATION NUMBER: 60/199,084  
: PRIOR FILING DATE: 2000-04-20  
: PRIOR APPLICATION NUMBER: 60/200,551

PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/202,278  
PRIOR FILING DATE: 2000-05-05  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PERL Program  
SEQ ID NO 3  
LENGTH: 451  
TYPE: PRF  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No: 3226980CD1  
PCT-US01-10436-3

Query Match 100.0%; Score 2318; DB 1; Length 451;  
Best Local Similarity 100.0%; Pred. No. 1.3e-207;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 361 KPAEEELRLPSREGSIEENFLQGTGCPSESWSRPLSPKOEPAVDPRIPGOIAE 420  
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DB 421 ETSEFLEQOLTSIDIMSDSYLRPAASPRLES 451

RESULT 2  
US-09-533-687-2

Sequence 2, Application US/09533687  
GENERAL INFORMATION:  
APPLICANT: Usman Shadon  
APPLICANT: Mahanandeshwar Gattu  
APPLICANT: David Michaelovich  
APPLICANT: Nabli Elshourbagy  
TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM RECEPTOR  
FILE REFERENCE: GP-70684  
CURRENT APPLICATION NUMBER: US/09/533,687  
CURRENT FILING DATE: 2000-03-23  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 451  
TYPE: PRF  
ORGANISM: HOMO SAPIENS  
US-09-533-687-2

Query Match 100.0%; Score 2318; DB 19; Length 451;

Best Local Similarity 100.0%; Pred. No. 1.3e-207;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 301 LPYFSFHLVYALSQPISTGQVESVTWIGYFCFTSNPFYGCINROIKELSKOFCVF 360  
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DB 361 KPAEEELRLPSREGSIEENFLQGTGCPSESWSRPLSPKOEPAVDPRIPGOIAE 420  
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DB 421 ETSEFLEQOLTSIDIMSDSYLRPAASPRLES 451

RESULT 3  
US-09-714-008A-12

Sequence 12, Application US/09714008A  
GENERAL INFORMATION:  
APPLICANT: Dang, Huong T.  
APPLICANT: Lowitz, Kevin P.  
TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled Receptors  
FILE REFERENCE: AREN0086  
CURRENT APPLICATION NUMBER: US/09/714,008A  
CURRENT FILING DATE: 2000-11-16  
Prior application data removed - consult PAM or file wrapper  
NUMBER OF SEQ ID NOS: 133  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 12  
LENGTH: 451  
TYPE: PRF  
ORGANISM: Homo sapiens  
US-09-714-008A-12

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Best Local Similarity 100.0%; Pred. No. 1.3e-207;  
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RESULT 4  
US-09-740-033-2

; Sequence 2, Application US/09740033  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF  
; FILE REFERENCE: C1001056  
; CURRENT APPLICATION NUMBER: US/09/740.033  
; CURRENT FILING DATE: 2000-12-20  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Human  
US-09-740-033-2

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Best Local Similarity 100.0%; Pred. No. 1,3e-207;  
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DB 121 LSVCFVSLALISVAINVERIYVYVHPMRKYEVRMTGLIVASVLGVWVKALAMASVPLG 180  
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DB 181 RVSMEGAPSVPPGCSLQMSHSAVCQLFVVVFAVLVFLPLLILVYVCSMFRAVARVAM 240  
QY 241 OHGPLPTMETPRORSESLSSRSTMTVSSGAPQTPHRTFGGKAAYVLLAVGGQFLLCW 300  
DB 241 OHGPLPTMETPRORSESLSSRSTMTVSSGAPQTPHRTFGGKAAYVLLAVGGQFLLCW 300  
QY 301 LPYFSFHLVYALSAQPISTGVGVSVTWIGYFCFTSNPFYGCINROI RIGELSKQVCFE 360  
DB 301 LPYFSFHLVYALSAQPISTGVGVSVTWIGYFCFTSNPFYGCINROI RIGELSKQVCFE 360  
QY 361 KPAPEEELRLPSRGCSIEENFLQLOGTGCPSSESVSRPLSPKQEPVAVDFRIPGOIAE 420  
DB 361 KPAPEEELRLPSRGCSIEENFLQLOGTGCPSSESVSRPLSPKQEPVAVDFRIPGOIAE 420  
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DB 421 ETSEFLQOULTSDIIMSDSYLRPAASPRLES 451

RESULT 5  
US-09-815-499-2

; Sequence 2, Application US/09815499  
; GENERAL INFORMATION:  
; APPLICANT: Elshourbagy, Nabli  
; APPLICANT: Gattu, Mahanandeeswar  
; APPLICANT: Michalovich, David  
; APPLICANT: Shabon, Usman  
; TITLE OF INVENTION: Molecular Cloning of a 7TM Receptor (AXOR64)  
; FILE REFERENCE: GB70684-1  
; CURRENT APPLICATION NUMBER: US/09/815.499  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: 09/533,687  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: GB 0027166.8  
; PRIOR FILING DATE: 2000-11-07  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-815-499-2

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Best Local Similarity 100.0%; Pred. No. 1,3e-207;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MESSPIPOSSGNSSTLGVNTPQPGSTASGVPEVGLRDVASEVALFPMILLDDITAVAGN 60  
QY 61 AAVNAVIKTPALRKRFVVFHLCIVDLALTLPLMLSSALFDHALFGEVACRYLTF 120  
DB 61 AAVNAVIKTPALRKRFVVFHLCIVDLALTLPLMLSSALFDHALFGEVACRYLTF 120  
QY 121 LSVCFVSLALISVAINVERIYVYVHPMRKYEVRMTGLIVASVLGVWVKALAMASVPLG 180  
DB 121 LSVCFVSLALISVAINVERIYVYVHPMRKYEVRMTGLIVASVLGVWVKALAMASVPLG 180  
QY 181 RVSMEGAPSVPPGCSLQMSHSAVCQLFVVVFAVLVFLPLLILVYVCSMFRAVARVAM 240  
DB 181 RVSMEGAPSVPPGCSLQMSHSAVCQLFVVVFAVLVFLPLLILVYVCSMFRAVARVAM 240  
QY 241 OHGPLPTMETPRORSESLSSRSTMTVSSGAPQTPHRTFGGKAAYVLLAVGGQFLLCW 300  
DB 241 OHGPLPTMETPRORSESLSSRSTMTVSSGAPQTPHRTFGGKAAYVLLAVGGQFLLCW 300  
QY 301 LPYFSFHLVYALSAQPISTGVGVSVTWIGYFCFTSNPFYGCINROI RIGELSKQVCFE 360  
DB 301 LPYFSFHLVYALSAQPISTGVGVSVTWIGYFCFTSNPFYGCINROI RIGELSKQVCFE 360  
QY 361 KPAPEEELRLPSRGCSIEENFLQLOGTGCPSSESVSRPLSPKQEPVAVDFRIPGOIAE 420  
DB 361 KPAPEEELRLPSRGCSIEENFLQLOGTGCPSSESVSRPLSPKQEPVAVDFRIPGOIAE 420  
QY 421 ETSEFLQOULTSDIIMSDSYLRPAASPRLES 451  
DB 421 ETSEFLQOULTSDIIMSDSYLRPAASPRLES 451

RESULT 6  
US-09-838-028-2

; Sequence 2, Application US/09838028  
; GENERAL INFORMATION:  
; APPLICANT: Lind, Peter  
; APPLICANT: Berthold, Malin  
; TITLE OF INVENTION: Novel G Protein-Coupled Receptor  
; FILE REFERENCE: 00125US2

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; CURRENT APPLICATION NUMBER: US/09/838,028
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 60/198,600
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-838-028-2

Query Match          100.0%; Score 2318; DB 22; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.3e-207;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTLGRVPTPGPSTASGVPEVGLRDVASESVALPFMLLDLTAAVAGN 60
    |||||||
DB 1 MESSPIPOSSGNSSTLGRVPTPGPSTASGVPEVGLRDVASESVALPFMLLDLTAAVAGN 60
    |||||||

QY 61 AAVNAVIKTPALRKFFVFPHLCVLDLALTLPLMLSSSALFDHALFGEVACRLYLF 120
    |||||||
DB 61 AAVNAVIKTPALRKFFVFPHLCVLDLALTLPLMLSSSALFDHALFGEVACRLYLF 120
    |||||||

QY 121 LSVCFVSLATLSVAIINVERYYYVHPMKRYEVRMTGLVASVLYGVWVKALAMASVPLYG 180
    |||||||
DB 121 LSVCFVSLATLSVAIINVERYYYVHPMKRYEVRMTGLVASVLYGVWVKALAMASVPLYG 180
    |||||||

QY 181 RVSWEEGAPSPVPCGSIQMSHSATCOLFVYVFAVLFLPLLLILVYCSMFRVARAAM 240
    |||||||
DB 181 RVSWEEGAPSPVPCGSIQMSHSATCOLFVYVFAVLFLPLLLILVYCSMFRVARAAM 240
    |||||||

QY 241 QHGPLPTWMETPRORSESLSSRSTMTSSGAPQTTPHRTFGGKAAYVLLAVGQFLLCW 300
    |||||||
DB 241 QHGPLPTWMETPRORSESLSSRSTMTSSGAPQTTPHRTFGGKAAYVLLAVGQFLLCW 300
    |||||||

QY 301 LPYFSFHLVYALSAQPISTGVESVVTWIGYFCTSNPFYGCINROIIGELSKQFCFF 360
    |||||||
DB 301 LPYFSFHLVYALSAQPISTGVESVVTWIGYFCTSNPFYGCINROIIGELSKQFCFF 360
    |||||||

QY 361 KPAPEEELRLPSREGSIEENFLQGTGCPSESWSRPLSPQDEPPAVDFRIPQIAE 420
    |||||||
DB 361 KPAPEEELRLPSREGSIEENFLQGTGCPSESWSRPLSPQDEPPAVDFRIPQIAE 420
    |||||||

QY 421 ETSEFLQQLTSDIIMSDSYLRPAASPRLES 451
    |||||||
DB 421 ETSEFLQQLTSDIIMSDSYLRPAASPRLES 451
    |||||||

RESULT 7
US-09-860-797-2
; Sequence 2, Application US/09860797
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Marilyn Evelyn Lewis
; APPLICANT: Nicola Melanle Robas
; TITLE OF INVENTION: Novel Polypeptide
; FILE REFERENCE: PCS10924APME
; CURRENT APPLICATION NUMBER: US/09/860,797
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: GB 0012248.1
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: GB 0107394.9
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/211,421
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/283,441
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-860-797-2

Query Match          100.0%; Score 2318; DB 22; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.3e-207;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTLGRVPTPGPSTASGVPEVGLRDVASESVALPFMLLDLTAAVAGN 60
    |||||||
DB 1 MESSPIPOSSGNSSTLGRVPTPGPSTASGVPEVGLRDVASESVALPFMLLDLTAAVAGN 60
    |||||||

QY 61 AAVNAVIKTPALRKFFVFPHLCVLDLALTLPLMLSSSALFDHALFGEVACRLYLF 120
    |||||||
DB 61 AAVNAVIKTPALRKFFVFPHLCVLDLALTLPLMLSSSALFDHALFGEVACRLYLF 120
    |||||||

QY 121 LSVCFVSLATLSVAIINVERYYYVHPMKRYEVRMTGLVASVLYGVWVKALAMASVPLYG 180
    |||||||
DB 121 LSVCFVSLATLSVAIINVERYYYVHPMKRYEVRMTGLVASVLYGVWVKALAMASVPLYG 180
    |||||||

QY 181 RVSWEEGAPSPVPCGSIQMSHSATCOLFVYVFAVLFLPLLLILVYCSMFRVARAAM 240
    |||||||
DB 181 RVSWEEGAPSPVPCGSIQMSHSATCOLFVYVFAVLFLPLLLILVYCSMFRVARAAM 240
    |||||||

QY 241 QHGPLPTWMETPRORSESLSSRSTMTSSGAPQTTPHRTFGGKAAYVLLAVGQFLLCW 300
    |||||||
DB 241 QHGPLPTWMETPRORSESLSSRSTMTSSGAPQTTPHRTFGGKAAYVLLAVGQFLLCW 300
    |||||||

QY 301 LPYFSFHLVYALSAQPISTGVESVVTWIGYFCTSNPFYGCINROIIGELSKQFCFF 360
    |||||||
DB 301 LPYFSFHLVYALSAQPISTGVESVVTWIGYFCTSNPFYGCINROIIGELSKQFCFF 360
    |||||||

QY 361 KPAPEEELRLPSREGSIEENFLQGTGCPSESWSRPLSPQDEPPAVDFRIPQIAE 420
    |||||||
DB 361 KPAPEEELRLPSREGSIEENFLQGTGCPSESWSRPLSPQDEPPAVDFRIPQIAE 420
    |||||||

QY 421 ETSEFLQQLTSDIIMSDSYLRPAASPRLES 451
    |||||||
DB 421 ETSEFLQQLTSDIIMSDSYLRPAASPRLES 451
    |||||||

RESULT 8
US-09-864-029-22
; Sequence 22, Application US/09864029
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchiernev, Velizar T.
; APPLICANT: Grose, William M.
; APPLICANT: Szekeres Jr., Edward S.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Gangoli, Esha A.
; APPLICANT: MacDougall, John R.
; APPLICANT: Stone, David J.
; APPLICANT: Smitson, Glenda
; TITLE OF INVENTION: NOVEL GPCR-LIKE PROTEINS AND NUCLEIC ACIDS ENCODING
; FILE REFERENCE: 21402-022
; CURRENT APPLICATION NUMBER: US/09/864,029
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/206,757
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 60/214,372
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/219,786
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/207,020
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/220,593
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;; PRIOR FILING DATE: 2000-07-25  
;; PRIOR APPLICATION NUMBER: 60/239,542  
;; PRIOR FILING DATE: 2000-10-10  
;; PRIOR APPLICATION NUMBER: 60/256,402  
;; PRIOR FILING DATE: 2000-12-18  
;; PRIOR APPLICATION NUMBER: 60/271,645  
;; PRIOR FILING DATE: 2001-02-26  
;; PRIOR APPLICATION NUMBER: 60/274,809  
;; PRIOR FILING DATE: 2001-03-09  
;; PRIOR APPLICATION NUMBER: 60/275,590  
;; PRIOR FILING DATE: 2001-03-13  
;; NUMBER OF SEQ ID NOS: 59  
;; SOFTWARE: Patent In Ver. 2.1  
;; SEQ ID NO: 22  
;; LENGTH: 451  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-864-029-22

Query Match 100.0%; Score 2318; DB 22; Length 451;  
Best Local Similarity 100.0%; Pred. No. 1.3e-207;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTLGRVPTGPSTAGVPEVGLRDVASESVALFFMLLDLTPAVAGN 60  
DB 1 MESSPIPOSSGNSSTLGRVPTGPSTAGVPEVGLRDVASESVALFFMLLDLTPAVAGN 60  
QY 61 AAVMAVIATPALRKFEVFEHCLVDLLAALTPLMLAMSSSALFDHALFGEVACRLYLE 120  
DB 61 AAVMAVIATPALRKFEVFEHCLVDLLAALTPLMLAMSSSALFDHALFGEVACRLYLE 120  
QY 121 LSVCFVSLAILLSAIVNERYYVYVHPMKYEVKMTGLVASLVGVWAKALMASVPLVG 180  
DB 121 LSVCFVSLAILLSAIVNERYYVYVHPMKYEVKMTGLVASLVGVWAKALMASVPLVG 180  
QY 181 RVSMEGAPSVPGCSLQMSHSAYCQLFVYVFAVLFLPLDLLLVYCSMFRVARVAM 240  
DB 181 RVSMEGAPSVPGCSLQMSHSAYCQLFVYVFAVLFLPLDLLLVYCSMFRVARVAM 240  
QY 241 QHGPLETWMETPRQSESLSSRSSTWYSSGAPQTPPHRTFGGKAAYVLLAVGGFLLCW 300  
DB 241 QHGPLETWMETPRQSESLSSRSSTWYSSGAPQTPPHRTFGGKAAYVLLAVGGFLLCW 300  
QY 301 LPYFSPHLVVALSAOPISIGOVESVYTWIGYCFISNPFYGCILNKQIRGELSKOVCFE 360  
DB 301 LPYFSPHLVVALSAOPISIGOVESVYTWIGYCFISNPFYGCILNKQIRGELSKOVCFE 360  
QY 361 KPAPEEELRLPREGSIEENFLQFLQGTGCPSESWSRPLSPKOEPPAVDFRIRIGQIAE 420  
DB 361 KPAPEEELRLPREGSIEENFLQFLQGTGCPSESWSRPLSPKOEPPAVDFRIRIGQIAE 420  
QY 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451  
DB 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451

## RESULT 9

US-09-980-049-3  
;; Sequence 3, Application US/09980049  
;; GENERAL INFORMATION:  
;; APPLICANT: INCYTE GENOMICS, INC.  
;; APPLICANT: POLICKY, Jennifer L.  
;; APPLICANT: TRIBOULEY, Catherine M.  
;; APPLICANT: TANG, Y. Tom  
;; APPLICANT: BAUGHN, Mariah R.  
;; APPLICANT: GRAUL, Richard  
;; APPLICANT: KHAN, Farrah A.  
;; APPLICANT: NGUYEN, Dannel B.  
;; APPLICANT: PATTERSON, Chandra  
;; APPLICANT: LAU, Preeti  
;; APPLICANT: AU-YOUNG, Janice  
;; APPLICANT: YANG, Junming  
;; APPLICANT: HAFALIA, April

;; APPLICANT: WALIA, Narinder K.  
;; APPLICANT: DAS, Debopriya  
;; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS  
;; FILE REFERENCE: PI-0072 PCT  
;; CURRENT APPLICATION NUMBER: US/09/980,049  
;; CURRENT FILING DATE: 2001-11-28  
;; PRIOR APPLICATION NUMBER: 60/193,051; 60/195,155; 60/199,084; 60/200,551; 60/202,2  
;; PRIOR FILING DATE: 2000-03-29; 2000-04-06; 2000-04-20; 2000-04-28; 2000-05-05  
;; NUMBER OF SEQ ID NOS: 12  
;; SOFTWARE: PERL Program  
;; SEQ ID NO: 3  
;; LENGTH: 451  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE: NAME/KEY: misc\_feature  
;; OTHER INFORMATION: Incyte ID NO: 3226980CD1  
US-09-980-049-3

Query Match 100.0%; Score 2318; DB 23; Length 451;  
Best Local Similarity 100.0%; Pred. No. 1.3e-207;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTLGRVPTGPSTAGVPEVGLRDVASESVALFFMLLDLTPAVAGN 60  
DB 1 MESSPIPOSSGNSSTLGRVPTGPSTAGVPEVGLRDVASESVALFFMLLDLTPAVAGN 60  
QY 61 AAVMAVIATPALRKFEVFEHCLVDLLAALTPLMLAMSSSALFDHALFGEVACRLYLE 120  
DB 61 AAVMAVIATPALRKFEVFEHCLVDLLAALTPLMLAMSSSALFDHALFGEVACRLYLE 120  
QY 121 LSVCFVSLAILLSAIVNERYYVYVHPMKYEVKMTGLVASLVGVWAKALMASVPLVG 180  
DB 121 LSVCFVSLAILLSAIVNERYYVYVHPMKYEVKMTGLVASLVGVWAKALMASVPLVG 180  
QY 181 RVSMEGAPSVPGCSLQMSHSAYCQLFVYVFAVLFLPLDLLLVYCSMFRVARVAM 240  
DB 181 RVSMEGAPSVPGCSLQMSHSAYCQLFVYVFAVLFLPLDLLLVYCSMFRVARVAM 240  
QY 241 QHGPLETWMETPRQSESLSSRSSTWYSSGAPQTPPHRTFGGKAAYVLLAVGGFLLCW 300  
DB 241 QHGPLETWMETPRQSESLSSRSSTWYSSGAPQTPPHRTFGGKAAYVLLAVGGFLLCW 300  
QY 301 LPYFSPHLVVALSAOPISIGOVESVYTWIGYCFISNPFYGCILNKQIRGELSKOVCFE 360  
DB 301 LPYFSPHLVVALSAOPISIGOVESVYTWIGYCFISNPFYGCILNKQIRGELSKOVCFE 360  
QY 361 KPAPEEELRLPREGSIEENFLQFLQGTGCPSESWSRPLSPKOEPPAVDFRIRIGQIAE 420  
DB 361 KPAPEEELRLPREGSIEENFLQFLQGTGCPSESWSRPLSPKOEPPAVDFRIRIGQIAE 420  
QY 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451  
DB 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451

## RESULT 10

US-09-995-543-12  
;; Sequence 12, Application US/09995543  
;; GENERAL INFORMATION:  
;; APPLICANT: Chen, Rupong  
;; APPLICANT: Dang, Huong T. T.  
;; APPLICANT: Lowitz, Kevin P. P.  
;; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupl  
;; FILE REFERENCE: Aren-0311  
;; CURRENT APPLICATION NUMBER: US/09/995,543  
;; CURRENT FILING DATE: 2001-11-27  
;; PRIOR APPLICATION NUMBER: 09/170,496  
;; PRIOR FILING DATE: 1998-10-13  
;; PRIOR APPLICATION NUMBER: 60/226,760  
;; PRIOR FILING DATE: 2000-08-21  
;; PRIOR APPLICATION NUMBER: 09/714,008



Db 361 KPAPEEELRLPSREGSIEENFLQGTGCPSESWSRPLSPKOEPPAVDFRIPGOIAE 420  
Qy 421 ETSEFLBOQLTSDIIMSDSYLRPASPRLES 451  
Db 421 ETSEFLBOQLTSDIIMSDSYLRPASPRLES 451

## RESULT 12

US-60-202-278-1  
; Sequence 1, Application US/60202278  
; GENERAL INFORMATION:  
; APPLICANT: Lai, Preeti  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Policky, Jennifer L.  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: PI-0088 P  
; CURRENT APPLICATION NUMBER: US/60/202, 278  
; CURRENT FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PERL Program  
; SEQ ID NO 1  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No: 3226980CD1  
US-60-202-278-1

Query Match 100.0%; Score 2318; DB 26; Length 451;  
Best Local Similarity 100.0%; Pred. No. 1.3e-207;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60  
Db 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60  
Qy 61 AAVMAVIAKTPALRKRFVFFHCLVDLLAALTMLPLAMLSALFDHALFGEVACRLYLF 120  
Db 61 AAVMAVIAKTPALRKRFVFFHCLVDLLAALTMLPLAMLSALFDHALFGEVACRLYLF 120  
Qy 121 LSVCFVSLALISVSAINVERYYVHPMKREYRMTLGLVASVYGVWVKALAMASVPYLG 180  
Db 121 LSVCFVSLALISVSAINVERYYVHPMKREYRMTLGLVASVYGVWVKALAMASVPYLG 180  
Qy 121 LSVCFVSLALISVSAINVERYYVHPMKREYRMTLGLVASVYGVWVKALAMASVPYLG 180  
Db 121 LSVCFVSLALISVSAINVERYYVHPMKREYRMTLGLVASVYGVWVKALAMASVPYLG 180  
Qy 181 RYSMEGAPSVPPGCSLQMSHSAYCOLFVVFAVLYFLPLLILLVYCSMFRVARVAM 240  
Db 181 RYSMEGAPSVPPGCSLQMSHSAYCOLFVVFAVLYFLPLLILLVYCSMFRVARVAM 240  
Qy 241 OHGPIPTWMEPRQSESLSRSTWVTSSGAPQTPHRTFGGKAAVLLAVGGFLLCW 300  
Db 241 OHGPIPTWMEPRQSESLSRSTWVTSSGAPQTPHRTFGGKAAVLLAVGGFLLCW 300  
Qy 301 LPYFSFHLHYVALSAQPISTGVESVVTWIGYFCFTSNPFYGCCLNRQIRGELSKEQVCF 360  
Db 301 LPYFSFHLHYVALSAQPISTGVESVVTWIGYFCFTSNPFYGCCLNRQIRGELSKEQVCF 360  
Qy 361 KPAPEEELRLPSREGSIEENFLQGTGCPSESWSRPLSPKOEPPAVDFRIPGOIAE 420  
Db 361 KPAPEEELRLPSREGSIEENFLQGTGCPSESWSRPLSPKOEPPAVDFRIPGOIAE 420  
Qy 421 ETSEFLBOQLTSDIIMSDSYLRPASPRLES 451  
Db 421 ETSEFLBOQLTSDIIMSDSYLRPASPRLES 451

## RESULT 13

US-60-317-661-2  
; Sequence 2, Application US/60317661  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,  
; TITLE OF INVENTION: HGPBMY32, EXPRESSED HIGHLY IN BRAIN TISSUE

; FILE REFERENCE: D0183 psp  
; CURRENT APPLICATION NUMBER: US/60/317, 661  
; CURRENT FILING DATE: 2001-09-06  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-317-661-2

Query Match 100.0%; Score 2318; DB 26; Length 451;  
Best Local Similarity 100.0%; Pred. No. 1.3e-207;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60  
Db 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60  
Qy 61 AAVMAVIAKTPALRKRFVFFHCLVDLLAALTMLPLAMLSALFDHALFGEVACRLYLF 120  
Db 61 AAVMAVIAKTPALRKRFVFFHCLVDLLAALTMLPLAMLSALFDHALFGEVACRLYLF 120  
Qy 121 LSVCFVSLALISVSAINVERYYVHPMKREYRMTLGLVASVYGVWVKALAMASVPYLG 180  
Db 121 LSVCFVSLALISVSAINVERYYVHPMKREYRMTLGLVASVYGVWVKALAMASVPYLG 180  
Qy 181 RYSMEGAPSVPPGCSLQMSHSAYCOLFVVFAVLYFLPLLILLVYCSMFRVARVAM 240  
Db 181 RYSMEGAPSVPPGCSLQMSHSAYCOLFVVFAVLYFLPLLILLVYCSMFRVARVAM 240  
Qy 241 OHGPIPTWMEPRQSESLSRSTWVTSSGAPQTPHRTFGGKAAVLLAVGGFLLCW 300  
Db 241 OHGPIPTWMEPRQSESLSRSTWVTSSGAPQTPHRTFGGKAAVLLAVGGFLLCW 300  
Qy 301 LPYFSFHLHYVALSAQPISTGVESVVTWIGYFCFTSNPFYGCCLNRQIRGELSKEQVCF 360  
Db 301 LPYFSFHLHYVALSAQPISTGVESVVTWIGYFCFTSNPFYGCCLNRQIRGELSKEQVCF 360  
Qy 361 KPAPEEELRLPSREGSIEENFLQGTGCPSESWSRPLSPKOEPPAVDFRIPGOIAE 420  
Db 361 KPAPEEELRLPSREGSIEENFLQGTGCPSESWSRPLSPKOEPPAVDFRIPGOIAE 420  
Qy 421 ETSEFLBOQLTSDIIMSDSYLRPASPRLES 451  
Db 421 ETSEFLBOQLTSDIIMSDSYLRPASPRLES 451

## RESULT 14

US-60-329-926-2  
; Sequence 2, Application US/60329926  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,  
; TITLE OF INVENTION: HGPBMY32, EXPRESSED HIGHLY IN BRAIN TISSUE  
; FILE REFERENCE: D0183 psp1  
; CURRENT APPLICATION NUMBER: US/60/329, 926  
; CURRENT FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-329-926-2

Query Match 100.0%; Score 2318; DB 26; Length 451;  
Best Local Similarity 100.0%; Pred. No. 1.3e-207;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60  
Db 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60

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Oy 61 AAVMAVIKTPALRKFEVFNHLCVLDLTLAALTLMPALMLSSALDFDHALFGEVACRLYLE 120
Db 61 AAVMAVIKTPALRKFEVFNHLCVLDLTLAALTLMPALMLSSALDFDHALFGEVACRLYLE 120
Oy 121 LSVCFVSLAILSVSAIINVERYYVYVHPMKREYRMTLGLVASVYGVWVKALAMASVPYLG 180
Db 121 LSVCFVSLAILSVSAIINVERYYVYVHPMKREYRMTLGLVASVYGVWVKALAMASVPYLG 180
Oy 181 RYSMEGAPSVPPGCSLQMSHSAQCOLFVYVFAVLVYFLPLLLILVYVCSMFRVARVAM 240
Db 181 RYSMEGAPSVPPGCSLQMSHSAQCOLFVYVFAVLVYFLPLLLILVYVCSMFRVARVAM 240
Oy 241 OHGPLPTWMEETPRORSESLSSRSTWVTSSGAPQTTPHRTFGGKAAYVLLAVGGQFLLCW 300
Db 241 OHGPLPTWMEETPRORSESLSSRSTWVTSSGAPQTTPHRTFGGKAAYVLLAVGGQFLLCW 300
Oy 301 LPYFSFHLVYVLSAOPISTGOVESVYTWIGYFCFTSNPFYGCILNRQIRGELSKQFVCFE 360
Db 301 LPYFSFHLVYVLSAOPISTGOVESVYTWIGYFCFTSNPFYGCILNRQIRGELSKQFVCFE 360
Oy 361 KPAPEELRLPSREGSIEENFLQFLOGTGCPSSEWSRPLSPKQEPVADFRIPQITAE 420
Db 361 KPAPEELRLPSREGSIEENFLQFLOGTGCPSSEWSRPLSPKQEPVADFRIPQITAE 420
Oy 421 ETSEFLQOLTSDIIMSDSYLRPASPRLES 451
Db 421 ETSEFLQOLTSDIIMSDSYLRPASPRLES 451
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## RESULT 15

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US-09-714-008A-100
: Sequence 100, Application US/09714008A
: GENERAL INFORMATION:
: APPLICANT: Dang, Huong T.
: APPLICANT: Lowitz, Kevin P.
: TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled
: FILE REFERENCE: AREN0086
: CURRENT APPLICATION NUMBER: US/09/714,008A
: PRIORITY FILING DATE: 2000-11-16
: PRIOR APPLICATION data removed - consult PALM or file wrapper
: SOFTWARE: Patent version 3.0
: SEQ ID NO 100
: LENGTH: 869
: TYPE: PRT
: ORGANISM: Homo sapiens and Rat
US-09-714-008A-100
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Query Match 100.0%; Score 2318; DB 21; Length 869;
Best Local Similarity 100.0%; Pred. No. 3,1e-207;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 MESSPIPOSSGNSSTLGRVPQTGPSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60
Db 1 MESSPIPOSSGNSSTLGRVPQTGPSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60
Oy 61 AAVMAVIKTPALRKFEVFNHLCVLDLTLAALTLMPALMLSSALDFDHALFGEVACRLYLE 120
Db 61 AAVMAVIKTPALRKFEVFNHLCVLDLTLAALTLMPALMLSSALDFDHALFGEVACRLYLE 120
Oy 121 LSVCFVSLAILSVSAIINVERYYVYVHPMKREYRMTLGLVASVYGVWVKALAMASVPYLG 180
Db 121 LSVCFVSLAILSVSAIINVERYYVYVHPMKREYRMTLGLVASVYGVWVKALAMASVPYLG 180
Oy 181 RYSMEGAPSVPPGCSLQMSHSAQCOLFVYVFAVLVYFLPLLLILVYVCSMFRVARVAM 240
Db 181 RYSMEGAPSVPPGCSLQMSHSAQCOLFVYVFAVLVYFLPLLLILVYVCSMFRVARVAM 240
Oy 241 OHGPLPTWMEETPRORSESLSSRSTWVTSSGAPQTTPHRTFGGKAAYVLLAVGGQFLLCW 300
Db 241 OHGPLPTWMEETPRORSESLSSRSTWVTSSGAPQTTPHRTFGGKAAYVLLAVGGQFLLCW 300
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Db 241 OHGPLPTWMEETPRORSESLSSRSTWVTSSGAPQTTPHRTFGGKAAYVLLAVGGQFLLCW 300
Oy 301 LPYFSFHLVYVLSAOPISTGOVESVYTWIGYFCFTSNPFYGCILNRQIRGELSKQFVCFE 360
Db 301 LPYFSFHLVYVLSAOPISTGOVESVYTWIGYFCFTSNPFYGCILNRQIRGELSKQFVCFE 360
Oy 361 KPAPEELRLPSREGSIEENFLQFLOGTGCPSSEWSRPLSPKQEPVADFRIPQITAE 420
Db 361 KPAPEELRLPSREGSIEENFLQFLOGTGCPSSEWSRPLSPKQEPVADFRIPQITAE 420
Oy 421 ETSEFLQOLTSDIIMSDSYLRPASPRLES 451
Db 421 ETSEFLQOLTSDIIMSDSYLRPASPRLES 451
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Search completed: October 21, 2002, 16:12:45
Job time : 116 secs
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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:09:30 : Search time 46 Seconds  
(without alignments)  
2767.495 Million cell updates/sec

Title: US-09-838-028-2

Perfect score: 2318  
Sequence: 1 MESSPIPOSSGNSSTIGLRVP.....SDIIMSDSYLRPAAPRLES 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1037649 seqs, 282272221 residues

Total number of hits satisfying chosen parameters: 1037649

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pending\_Patents\_AA\_New:\*  
2: /cgn2\_6/ptodata/1/paa/PCIT\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep:\*  
8: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2318	100.0	451	1 PCT-US01-03162-2	Sequence 2, Appl1
2	2318	100.0	451	5 US-09-891-138-12	Sequence 12, Appl1
3	2318	100.0	451	5 US-09-891-138A-12	Sequence 12, Appl1
4	2318	100.0	451	6 US-10-088-726-18	Sequence 18, Appl1
5	2318	100.0	451	6 US-10-079-384-2	Sequence 2, Appl1
6	2318	100.0	451	6 US-10-221-160-2	Sequence 2, Appl1
7	2106	90.9	417	6 US-10-219-834-73	Sequence 73, Appl1
8	1276	55.0	252	6 US-10-219-834-74	Sequence 74, Appl1
9	677	29.2	143	6 US-10-221-279-10303	Sequence 10303, A
10	438.5	18.9	368	6 US-10-125-749-10	Sequence 10, Appl1
11	438.5	18.9	368	6 US-10-070-334-1	Sequence 1, Appl1
12	438.5	18.9	368	6 US-10-220-382-4	Sequence 4, Appl1
13	347	15.0	348	7 US-60-389-987-208	Sequence 208, App
14	347	15.0	348	7 US-60-412-418-208	Sequence 208, App
15	337	14.5	400	5 US-09-546-038A-31	Sequence 31, Appl1
16	333	14.4	565	6 US-10-130-461-12	Sequence 12, Appl1
17	332.5	14.3	572	6 US-10-185-991-2	Sequence 2, Appl1
18	332.5	14.3	572	6 US-10-238-129-2	Sequence 2, Appl1
19	332.5	14.3	572	6 US-10-238-667-2	Sequence 2, Appl1
20	325	14.0	501	6 US-10-238-129-7	Sequence 7, Appl1
21	325	14.0	501	6 US-10-238-667-7	Sequence 7, Appl1
22	322.5	13.9	560	6 US-10-238-129-8	Sequence 8, Appl1
23	322.5	13.9	560	6 US-10-238-667-8	Sequence 8, Appl1
24	319.5	13.8	402	7 US-60-389-987-59	Sequence 59, Appl1
25	319.5	13.8	402	7 US-60-412-418-59	Sequence 59, Appl1
26	310	13.4	515	6 US-10-238-129-9	Sequence 9, Appl1

27	310	13.4	515	6 US-10-238-667-9	Sequence 9, Appl1
28	308	13.3	515	6 US-10-130-461-11	Sequence 11, Appl1
29	308	13.3	520	6 US-10-185-991-4	Sequence 4, Appl1
30	308	13.3	520	6 US-10-238-129-4	Sequence 4, Appl1
31	308	13.3	520	6 US-10-238-667-4	Sequence 4, Appl1
32	306	13.2	466	1 PCT-US02-25319-26	Sequence 26, Appl1
33	306	13.2	466	5 US-09-952-680A-26	Sequence 26, Appl1
34	306	13.2	466	6 US-10-002-945-129	Sequence 129, Appl1
35	306	13.2	466	6 US-10-215-982-26	Sequence 26, Appl1
36	305	13.2	497	5 US-09-568-255-2	Sequence 2, Appl1
37	305	13.2	497	6 US-10-052-589-2	Sequence 2, Appl1
38	305	13.2	515	6 US-10-238-129-10	Sequence 10, Appl1
39	305	13.2	515	6 US-10-238-667-10	Sequence 10, Appl1
40	300.5	13.0	466	5 US-60-380-336-49	Sequence 49, Appl1
41	300	12.9	429	5 US-09-919-039-6	Sequence 6, Appl1
42	300	12.9	466	6 US-10-130-461-10	Sequence 10, Appl1
43	300	12.9	466	6 US-10-185-991-6	Sequence 6, Appl1
44	300	12.9	466	6 US-10-238-129-6	Sequence 6, Appl1
45	300	12.9	466	6 US-10-238-667-6	Sequence 6, Appl1

#### ALIGNMENTS

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RESULT 1
PCT-US01-03162-2
Sequence 2, Application PC/TUS0103162
GENERAL INFORMATION:
APPLICANT: Shyman Ramakrishnan
TITLE OF INVENTION: REGULATION OF HUMAN HISTAMINE H2-LIKE G PROTEIN-COUPLED
TITLE OF INVENTION: RECEPTOR
FILE REFERENCE: 004974.00792
CURRENT APPLICATION NUMBER: PCT/US01/03162
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/190,554
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 60/210,734
PRIOR FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: 60/255,147
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 451
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-03162-2
Query Match 100.0% Score 2318; DB 1; Length 451;
Best Local Similarity 100.0% Pred No. 5.3e-185;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MESSPIPOSSGNSSTIGLRVPQTGPSTASGVPEGLRDVASSEVALFFMLLDLTAVAGN 60
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DB 1 MESSPIPOSSGNSSTIGLRVPQTGPSTASGVPEGLRDVASSEVALFFMLLDLTAVAGN 60
QY 61 AAWAVYAKTPALRKFFVPHCLVDLLALTLPLAMSSSLFDHALGFEVACRLYLE 120
|||||
DB 61 AAWAVYAKTPALRKFFVPHCLVDLLALTLPLAMSSSLFDHALGFEVACRLYLE 120
QY 121 LSVCFYSALTSVAIVERYYVYVHPMYREVMNTGLVASVYGVWVKALMAASPVIG 180
|||||
DB 121 LSVCFYSALTSVAIVERYYVYVHPMYREVMNTGLVASVYGVWVKALMAASPVIG 180
QY 181 RVSMGAPSPVPGCSLQMSHAYCOLFVVVFVFLPLLLILVYCSMPFVAVVAM 240
|||||
DB 181 RVSMGAPSPVPGCSLQMSHAYCOLFVVVFVFLPLLLILVYCSMPFVAVVAM 240
QY 241 QHPLPLTWMTTPQREBSLSSRTMYTSSGAPOTTTHRTFGGKAAYVLLAVGGQFLCW 300
|||||
DB 241 QHPLPLTWMTTPQREBSLSSRTMYTSSGAPOTTTHRTFGGKAAYVLLAVGGQFLCW 300
QY 301 LPYFSHLVVALSAQPISTGQVSVVTWIGYPCFTSNPFYGLNQLNGELSKQVCF 360
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Db 301 LPYFSFHLVYVLSAQPISITGQVESVVTWIGYFCFTSNPFYGCINROI RGLSKQFVCF 360  
Qy 361 KPAPEEELRLPSRGSIENFLQIQTGCGPSESWSRPLSPKQEPVAVDFRIPQIAE 420  
Db 361 KPAPEEELRLPSRGSIENFLQIQTGCGPSESWSRPLSPKQEPVAVDFRIPQIAE 420  
Qy 421 ETSEFLQQLTSDITMSDSYLRPAASPRLES 451  
Db 421 ETSEFLQQLTSDITMSDSYLRPAASPRLES 451

RESULT 2  
US-09-891-138-12  
Sequence 12, Application US/09891138  
GENERAL INFORMATION:  
APPLICANT: Lin, Daniel Chi-Hong  
APPLICANT: Zhao, Jiaqiang  
APPLICANT: Chen, Jin-Long  
APPLICANT: Cutler, Gene  
APPLICANT: Tularik Inc.  
TITLE OF INVENTION: Novel Receptors  
FILE REFERENCE: 018781-006210US  
CURRENT APPLICATION NUMBER: US/09/891,138  
CURRENT FILING DATE: 2001-06-25  
PRIOR APPLICATION NUMBER: US 60/213,461  
PRIOR FILING DATE: 2000-06-23  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 12  
LENGTH: 451  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human TGR213 G-protein coupled receptor (GPCR)  
US-09-891-138-12

Query Match 100.0%; Score 2318; DB 5; Length 451;  
Best Local Similarity 100.0%; Pred. No. 5, 3e-185;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESSPIPOSSGNSSTLGRVDPQPGSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60  
Db 1 MESSPIPOSSGNSSTLGRVDPQPGSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60  
Qy 61 AAVAAVIAKTPALRKFEVFFHLCLVDLLAALTLPMLAMSSALFDHALFGEVACRLYLF 120  
Db 61 AAVAAVIAKTPALRKFEVFFHLCLVDLLAALTLPMLAMSSALFDHALFGEVACRLYLF 120  
Qy 121 LSVCFVSLAITSVAIINERYYYVHPMRYEVRMTGLVASLVGVWVKALAMASVPVLG 180  
Db 121 LSVCFVSLAITSVAIINERYYYVHPMRYEVRMTGLVASLVGVWVKALAMASVPVLG 180  
Qy 181 RVSMEEGASVPVPCGSLQWSHSAYCOLFVVFAVLYFLPLLILVYVCSMFVAVAAAM 240  
Db 181 RVSMEEGASVPVPCGSLQWSHSAYCOLFVVFAVLYFLPLLILVYVCSMFVAVAAAM 240  
Qy 241 OHGPLPTMMETPRORSLSRSTMTVSSGAPQTPHRTFGGKAAYVLLAVGGQFLLCW 300  
Db 241 OHGPLPTMMETPRORSLSRSTMTVSSGAPQTPHRTFGGKAAYVLLAVGGQFLLCW 300  
Qy 301 LPYFSFHLVYVLSAQPISITGQVESVVTWIGYFCFTSNPFYGCINROI RGLSKQFVCF 360  
Db 301 LPYFSFHLVYVLSAQPISITGQVESVVTWIGYFCFTSNPFYGCINROI RGLSKQFVCF 360  
Qy 361 KPAPEEELRLPSRGSIENFLQIQTGCGPSESWSRPLSPKQEPVAVDFRIPQIAE 420  
Db 361 KPAPEEELRLPSRGSIENFLQIQTGCGPSESWSRPLSPKQEPVAVDFRIPQIAE 420  
Qy 421 ETSEFLQQLTSDITMSDSYLRPAASPRLES 451  
Db 421 ETSEFLQQLTSDITMSDSYLRPAASPRLES 451

RESULT 3  
US-09-891-138A-12  
Sequence 12, Application US/09891138A  
GENERAL INFORMATION:  
APPLICANT: Lin, Daniel Chi-Hong  
APPLICANT: Zhao, Jiaqiang  
APPLICANT: Chen, Jin-Long  
APPLICANT: Cutler, Gene  
APPLICANT: Tularik Inc.  
TITLE OF INVENTION: Novel Receptors  
FILE REFERENCE: 018781-006210US  
CURRENT APPLICATION NUMBER: US/09/891,138A  
CURRENT FILING DATE: 2001-06-25  
PRIOR APPLICATION NUMBER: US 60/213,461  
PRIOR FILING DATE: 2000-06-23  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 12  
LENGTH: 451  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human TGR213 G-protein coupled receptor (GPCR)  
US-09-891-138A-12

Query Match 100.0%; Score 2318; DB 5; Length 451;  
Best Local Similarity 100.0%; Pred. No. 5, 3e-185;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESSPIPOSSGNSSTLGRVDPQPGSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60  
Db 1 MESSPIPOSSGNSSTLGRVDPQPGSTASGVPEVGLRDVASESVALFFMLLDLTAVAGN 60  
Qy 61 AAVAAVIAKTPALRKFEVFFHLCLVDLLAALTLPMLAMSSALFDHALFGEVACRLYLF 120  
Db 61 AAVAAVIAKTPALRKFEVFFHLCLVDLLAALTLPMLAMSSALFDHALFGEVACRLYLF 120  
Qy 121 LSVCFVSLAITSVAIINERYYYVHPMRYEVRMTGLVASLVGVWVKALAMASVPVLG 180  
Db 121 LSVCFVSLAITSVAIINERYYYVHPMRYEVRMTGLVASLVGVWVKALAMASVPVLG 180  
Qy 181 RVSMEEGASVPVPCGSLQWSHSAYCOLFVVFAVLYFLPLLILVYVCSMFVAVAAAM 240  
Db 181 RVSMEEGASVPVPCGSLQWSHSAYCOLFVVFAVLYFLPLLILVYVCSMFVAVAAAM 240  
Qy 241 OHGPLPTMMETPRORSLSRSTMTVSSGAPQTPHRTFGGKAAYVLLAVGGQFLLCW 300  
Db 241 OHGPLPTMMETPRORSLSRSTMTVSSGAPQTPHRTFGGKAAYVLLAVGGQFLLCW 300  
Qy 301 LPYFSFHLVYVLSAQPISITGQVESVVTWIGYFCFTSNPFYGCINROI RGLSKQFVCF 360  
Db 301 LPYFSFHLVYVLSAQPISITGQVESVVTWIGYFCFTSNPFYGCINROI RGLSKQFVCF 360  
Qy 361 KPAPEEELRLPSRGSIENFLQIQTGCGPSESWSRPLSPKQEPVAVDFRIPQIAE 420  
Db 361 KPAPEEELRLPSRGSIENFLQIQTGCGPSESWSRPLSPKQEPVAVDFRIPQIAE 420  
Qy 421 ETSEFLQQLTSDITMSDSYLRPAASPRLES 451  
Db 421 ETSEFLQQLTSDITMSDSYLRPAASPRLES 451

RESULT 4  
US-10-088-726-18  
Sequence 18, Application US/10088726  
GENERAL INFORMATION:  
APPLICANT: Matsumoto et al.  
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE-BINDING PROTEIN-COUPLED RECEPTORS  
FILE REFERENCE: 62514  
CURRENT APPLICATION NUMBER: US/10/088,726  
CURRENT FILING DATE: 2002-03-22



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: PRIOR APPLICATION NUMBER: PCT/JP00/09408
: PRIOR FILING DATE: 2000-12-28      1999-375152
: PRIOR APPLICATION NUMBER: JP
: PRIOR FILING DATE: 1999-12-28
: PRIOR APPLICATION NUMBER: JP      2000-101339
: PRIOR FILING DATE: 2000-03-31
: NUMBER OF SEQ ID NOS: 63
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 18
: LENGTH: 451
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-088-726-18

Query Match      100.0%: Score 2318; DB 6; Length 451;
Best Local Similarity 100.0%; Pred. No. 5.3e-185;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTLGRVPOTPGPSTASGVPEVGLRDVASSEVALFEMLLDITLAVAGN 60
DB 1 MESSPIPOSSGNSSTLGRVPOTPGPSTASGVPEVGLRDVASSEVALFEMLLDITLAVAGN 60
QY 61 AAVMAVIAKTPALRKRFVFEVHCLVDLLAALTLMPLAMLSSSALPDHALFGEVACRLYLE 120
DB 61 AAVMAVIAKTPALRKRFVFEVHCLVDLLAALTLMPLAMLSSSALPDHALFGEVACRLYLE 120
QY 121 LSVCFVSLALISVSAIINVERYYVHPMKREYRMTLGLVASVVGWVKALAMASVPVLG 180
DB 121 LSVCFVSLALISVSAIINVERYYVHPMKREYRMTLGLVASVVGWVKALAMASVPVLG 180
QY 181 RVSMEGAPSVPPGCSLQMSHSAQCQLFVYVFAVLYFLPLLIIIVYCSMRVARVAM 240
DB 181 RVSMEGAPSVPPGCSLQMSHSAQCQLFVYVFAVLYFLPLLIIIVYCSMRVARVAM 240
QY 241 OHGPLPTMNETPRQRESLSRSRTWTSAGAPQTPHRTFGGKAAYVLLAVGGOFLLCW 300
DB 241 OHGPLPTMNETPRQRESLSRSRTWTSAGAPQTPHRTFGGKAAYVLLAVGGOFLLCW 300
QY 301 LPYFSEHLYVALSAPISTGVESVVTWIGYFCFTSNPFYGCINRQIRGELSKQVCFE 360
DB 301 LPYFSEHLYVALSAPISTGVESVVTWIGYFCFTSNPFYGCINRQIRGELSKQVCFE 360
QY 361 KPAPEEELRLPSREGSIEENFLQFLOGTCGCPSESWSRPLSPKQEPRAVDPRIRIGQIAE 420
DB 361 KPAPEEELRLPSREGSIEENFLQFLOGTCGCPSESWSRPLSPKQEPRAVDPRIRIGQIAE 420
QY 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451
DB 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451

RESULT 5
US-10-079-384-2
: Sequence 2, Application US/10079384
: GENERAL INFORMATION:
: APPLICANT: Communi, Didier
: TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
: FILE REFERENCE: 9409/2132
: CURRENT APPLICATION NUMBER: US/10/079,384
: CURRENT FILING DATE: 2002-02-20
: PRIOR APPLICATION NUMBER: US 09/885,453
: PRIOR FILING DATE: 2001-06-20
: NUMBER OF SEQ ID NOS: 50
: SOFTWARE: Patent In version 3.1
: SEQ ID NO 2
: LENGTH: 451
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-079-384-2

Query Match      100.0%: Score 2318; DB 6; Length 451;
Best Local Similarity 100.0%; Pred. No. 5.3e-185;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTLGRVPOTPGPSTASGVPEVGLRDVASSEVALFEMLLDITLAVAGN 60
DB 1 MESSPIPOSSGNSSTLGRVPOTPGPSTASGVPEVGLRDVASSEVALFEMLLDITLAVAGN 60
QY 61 AAVMAVIAKTPALRKRFVFEVHCLVDLLAALTLMPLAMLSSSALPDHALFGEVACRLYLE 120
DB 61 AAVMAVIAKTPALRKRFVFEVHCLVDLLAALTLMPLAMLSSSALPDHALFGEVACRLYLE 120
QY 121 LSVCFVSLALISVSAIINVERYYVHPMKREYRMTLGLVASVVGWVKALAMASVPVLG 180
DB 121 LSVCFVSLALISVSAIINVERYYVHPMKREYRMTLGLVASVVGWVKALAMASVPVLG 180
QY 181 RVSMEGAPSVPPGCSLQMSHSAQCQLFVYVFAVLYFLPLLIIIVYCSMRVARVAM 240
DB 181 RVSMEGAPSVPPGCSLQMSHSAQCQLFVYVFAVLYFLPLLIIIVYCSMRVARVAM 240
QY 241 OHGPLPTMNETPRQRESLSRSRTWTSAGAPQTPHRTFGGKAAYVLLAVGGOFLLCW 300
DB 241 OHGPLPTMNETPRQRESLSRSRTWTSAGAPQTPHRTFGGKAAYVLLAVGGOFLLCW 300
QY 301 LPYFSEHLYVALSAPISTGVESVVTWIGYFCFTSNPFYGCINRQIRGELSKQVCFE 360
DB 301 LPYFSEHLYVALSAPISTGVESVVTWIGYFCFTSNPFYGCINRQIRGELSKQVCFE 360
QY 361 KPAPEEELRLPSREGSIEENFLQFLOGTCGCPSESWSRPLSPKQEPRAVDPRIRIGQIAE 420
DB 361 KPAPEEELRLPSREGSIEENFLQFLOGTCGCPSESWSRPLSPKQEPRAVDPRIRIGQIAE 420
QY 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451
DB 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451

RESULT 6
US-10-221-160-2
: Sequence 2, Application US/10221160
: GENERAL INFORMATION:
: APPLICANT: Shyman Ramakrishnan
: TITLE OF INVENTION: REGULATION OF HUMAN SEROTONIN-LIKE G PROTEIN-COUPLED
: FILE REFERENCE: 004974.00791
: CURRENT APPLICATION NUMBER: US/10/221,160
: CURRENT FILING DATE: 2002-09-18
: PRIOR APPLICATION NUMBER: US 60/190,194
: PRIOR FILING DATE: 2000-03-20
: PRIOR APPLICATION NUMBER: US 60/210,975
: PRIOR FILING DATE: 2000-06-12
: PRIOR APPLICATION NUMBER: US 60/255,110
: PRIOR FILING DATE: 2000-12-14
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 2
: LENGTH: 451
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-221-160-2

Query Match      100.0%: Score 2318; DB 6; Length 451;
Best Local Similarity 100.0%; Pred. No. 5.3e-185;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTLGRVPOTPGPSTASGVPEVGLRDVASSEVALFEMLLDITLAVAGN 60
DB 1 MESSPIPOSSGNSSTLGRVPOTPGPSTASGVPEVGLRDVASSEVALFEMLLDITLAVAGN 60
QY 61 AAVMAVIAKTPALRKRFVFEVHCLVDLLAALTLMPLAMLSSSALPDHALFGEVACRLYLE 120
DB 61 AAVMAVIAKTPALRKRFVFEVHCLVDLLAALTLMPLAMLSSSALPDHALFGEVACRLYLE 120
QY 121 LSVCFVSLALISVSAIINVERYYVHPMKREYRMTLGLVASVVGWVKALAMASVPVLG 180
DB 121 LSVCFVSLALISVSAIINVERYYVHPMKREYRMTLGLVASVVGWVKALAMASVPVLG 180
QY 181 RVSMEGAPSVPPGCSLQMSHSAQCQLFVYVFAVLYFLPLLIIIVYCSMRVARVAM 240
DB 181 RVSMEGAPSVPPGCSLQMSHSAQCQLFVYVFAVLYFLPLLIIIVYCSMRVARVAM 240
QY 241 OHGPLPTMNETPRQRESLSRSRTWTSAGAPQTPHRTFGGKAAYVLLAVGGOFLLCW 300
DB 241 OHGPLPTMNETPRQRESLSRSRTWTSAGAPQTPHRTFGGKAAYVLLAVGGOFLLCW 300
QY 301 LPYFSEHLYVALSAPISTGVESVVTWIGYFCFTSNPFYGCINRQIRGELSKQVCFE 360
DB 301 LPYFSEHLYVALSAPISTGVESVVTWIGYFCFTSNPFYGCINRQIRGELSKQVCFE 360
QY 361 KPAPEEELRLPSREGSIEENFLQFLOGTCGCPSESWSRPLSPKQEPRAVDPRIRIGQIAE 420
DB 361 KPAPEEELRLPSREGSIEENFLQFLOGTCGCPSESWSRPLSPKQEPRAVDPRIRIGQIAE 420
QY 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451
DB 421 ETSEFLEOQLTSDIIMSDSYLRPAASPRLES 451
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;; CURRENT FILING DATE: 2002-09-06  
;; PRIOR APPLICATION NUMBER: 09/574,454  
;; PRIOR FILING DATE: 2000-05-19  
;; PRIOR APPLICATION NUMBER: 09/519,705  
;; PRIOR FILING DATE: 2000-03-07  
;; NUMBER OF SEQ ID NOS: 12360  
;; SOFTWARE: Custom  
;; SEQ ID NO 10303  
;; LENGTH: 143  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-221-279-10303

Query Match 29.2%; Score 677; DB 6; Length 143;  
Best Local Similarity 95.5%; Pred. No. 1.2e-48;  
Matches 126; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 313 SNAPISTGVESVVMIGFYCFSTSNPFYGCINROI RGLSKQFVCFKPADEELRLPS 372  
DB 1 SNAPISTGVESVVMIGFYCFSTSNPFYGCINROI RGLSKQFVCFKPADEELRLPS 60  
QY 373 REGSIEENFLQCTGCPSESWSRPLPSKQEPAPVDFRIPGOIAETSEFLDQULTS 432  
DB 61 REGSIEENFLQCTGCPSESWSRPLPSKQEPAPVDFRIPGOIAETSEFLDQULTS 120  
QY 433 DIIMSXYLRPA 444  
DB 121 DVIITNSYLSPA 132

RESULT 10  
US-10-125-749-10

;; Sequence 10, Application US/10125749  
;; GENERAL INFORMATION:

;; APPLICANT: Erding Hu  
;; APPLICANT: Yuan Zhu  
;; APPLICANT: Ganesh M. Sathe  
;; APPLICANT: Joyce Yue Mao  
;; APPLICANT: Wendy S. Halsey  
;; APPLICANT: Jon Chambers  
;; APPLICANT: Allison Isobel Muir  
;; APPLICANT: Philip Graham Szekeres  
;; APPLICANT: Usman Shabon  
;; APPLICANT: Derek J. Bergsma  
;; APPLICANT: Nabil A. Elshourbagy  
;; APPLICANT: David Michalovich  
;; APPLICANT: Pamela A. Lane  
;; APPLICANT: Menelaos N. Pangalos  
;; APPLICANT: Melanie Robbins  
;; APPLICANT: David Malcolm Duckworth  
;; APPLICANT: Jeffrey Hill  
;; APPLICANT: Ping Tsui  
;; APPLICANT: Pankaj Agarwal  
;; APPLICANT: Randall Forrest Smith  
;; APPLICANT: Lisa Vawter  
;; APPLICANT: Catherine E. Ellis  
;; APPLICANT: Manmandeshwar Gattu  
;; APPLICANT: John W. Quillen, Jr.  
;; APPLICANT: Erin M. Toland  
;; APPLICANT: Steven Michael Foord  
;; APPLICANT: Han Ngoc Trinh  
;; APPLICANT: Alexander Taylor  
;; APPLICANT: Henry Sarau  
;; APPLICANT: Steven Ruben  
;; APPLICANT: George H. Poste  
;; APPLICANT: Michel Louis Souchet  
;; APPLICANT: Philippe Laurent Robert  
;; APPLICANT: Stephane Clement Krief  
;; APPLICANT: Bernard Emile Joseph Gout  
;; APPLICANT: Eve Mahe  
;; TITLE OF INVENTION: HUMAN G PROTEIN-COUPLED RECEPTOR  
;; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
;; FILE REFERENCE: GP-70775B-C1

;; CURRENT APPLICATION NUMBER: US/10/125,749  
;; CURRENT FILING DATE: 2002-04-18  
;; PRIOR APPLICATION NUMBER: US/09/988,922  
;; PRIOR FILING DATE: 2001-11-19  
;; NUMBER OF SEQ ID NOS: 82  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 10  
;; LENGTH: 368  
;; TYPE: PRT  
;; ORGANISM: HOMO SAPIENS  
US-10-125-749-10

Query Match 18.9%; Score 438.5; DB 6; Length 368;  
Best Local Similarity 31.8%; Pred. No. 2.9e-28;  
Matches 127; Conservative 55; Mismatches 146; Indels 71; Gaps 14;

QY 40 ASE---SVALFPMLLDLTAVAGNAVMVIAKTPALRKFFVVFHLCVLDLALTLML 96  
DB 9 ASEVAGSIGLLIAAVEGALLNGALLVVRTGRLALYHLACVVDLLAASIMPL 68  
QY 97 AMLSSAL-FDHALFGEVACRLYLFLSVCFVSLAILLSAIVERIYYVHPMKREVRMT 155  
DB 69 GLIAAPPDGLGRVRLGPAPCARARELSAALLPACTLGVALLIARILVHPLRGSSRP 128  
QY 156 LGLVASVLGVVWKALAMASVPLGRVSWEGAPSVPPCCSLQWSHSAVCOL-----F 208  
DB 129 PVL---VLTAVMAAGLGLSL-----GPPAPPA-----PARCSVLAGLCP 172  
QY 209 VVFAVLYFLPLLLILVYCSMPFRVAVAMOHGPLPTMETPPRORESLSRSTMYTS 268  
DB 173 RPLMALFLALPALLLLGAYGIFVYARRAALR-PPRA--RGSRLRSDLSRLSIL-- 227  
QY 269 SGAPOTTPHRTGGKAAVYLLAVGGQFLCMLPFPSFLHYALSNAPISTGVESVVM 328  
DB 228 ---PPLRPR--LPGKAALAPALAVGQFAACWLPY----GCACLAARAAEAABAATW 277  
QY 329 IGYFCFTSNPFYGCINROI R--GELSKQFVCFKPADEELRLPSREGSIEENFLQFL 385  
DB 278 VAYSAPAAHPFLYGLQRPVRLALGRLSRRAL----PGVVR----- 314  
QY 386 OCTGCPSESWSRPLPSKQEPAPVDFRIPGOIAETSE 424  
DB 315 ---ACTPQAMHPRALLQCGRPBPBPVGPSPAPSPOTPE 350

RESULT 11  
US-10-070-334-1

;; Sequence 1, Application US/10070334  
;; GENERAL INFORMATION:

;; APPLICANT: WATANABE, TAKUYA  
;; APPLICANT: KIKUCHI, KUNIKO  
;; APPLICANT: SHINTANI, YASUSHI  
;; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR PROTEIN AND DNA  
;; FILE REFERENCE: 57126(46342)  
;; CURRENT APPLICATION NUMBER: US/10/070,334  
;; CURRENT FILING DATE: 2002-07-12  
;; PRIOR APPLICATION NUMBER: PCT/JP00/05663  
;; PRIOR FILING DATE: 2000-08-08  
;; PRIOR APPLICATION NUMBER: JP 11-241529  
;; PRIOR FILING DATE: 1999-08-27  
;; NUMBER OF SEQ ID NOS: 7  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 1  
;; LENGTH: 368  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-070-334-1

Query Match 18.9%; Score 438.5; DB 6; Length 368;  
Best Local Similarity 31.8%; Pred. No. 2.9e-28;  
Matches 127; Conservative 55; Mismatches 146; Indels 71; Gaps 14;

```

Oy 40 ASE---SWALEFEMLLDDTAAVGAANAAMAYIAKPARLKKEVFNFHCTVDLLAALTMPL 96
Db 9 ASEVAGSIGLGLAAVVEYGALGNGALGVVYLRTPGRLDYLHNLCVDVLLAAASTMPL 68
Oy 97 AMSSSAL-FDHALFGEVACRLYFLFSVCFSVALTSVSAINVERYYVVVNHPRAYEVRMT 155
Db 69 GLLAAPRGGLGRVRLGRPCSAARFELSAALLPACTGLVAGLARYLYIHLRPGSRPP 128
Oy 156 LGLVASYLVGVWYKALAMASYPVULGRVSWEBGAPSVPPGSLOWSHSAYQL-----F 208
Db 129 PVL---VLTAVMAAAGLGLALSTL-----GPRPAPPPA-----PARCSYLAGGLGPR 172
Oy 209 VVVFVAYLELLPRLLLIVVYCSMFRRVAVYAMONGRLPTMHETPRORSESSRSMTYMS 268
Db 173 RPLMLALFALPRLLLLGANGGITFVARRAALR-PRPPA---KGSRLKSDSLDRSLTL- 227
Oy 269 SGAROTTPHRTFFGGGKAAYVLLAAGGOFLLCMLRPFSEFHLVYVLSAOPISTGVESVYTW 328
Db 228 ---PPLRRR-LPGKKAALPALVAGGFACMWLP-----GCACSLAPAAAGALEAAVYW 277
Oy 329 IGYCFCTSNPFYVCCLNROIR---GELSKVCFCEFKPAPEEELRLPSREGSIEENFLOFL 385
Db 278 VAYSAFAHPRFLYGLLDRPVYALAGRSRLAL---PGPVR----- 314
Oy 386 QGTGCRPSSESWSRPLSPKOPRAPVDRIRIGQIAEENESE 424
Db 315 ---ACTPQAMHPRALLDCCLOLRPPRGAPVGBEAREOPIRE 350

```

RESULT 12  
US-10-220-382-4

```

Sequence 4 Application US/10220382
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: IAL, Preeti
APPLICANT: TANG, Y. Tom
APPLICANT: PATTERSON, Chandra
APPLICANT: VAO, Monique G.
APPLICANT: SHIH, Leo L.
APPLICANT: TRIBOULEY, Catherine
APPLICANT: LU, Dying Anna M.
APPLICANT: YUE, Henry
APPLICANT: KHAN, Farrah A.
APPLICANT: POLICKY, Jennifer L.
APPLICANT: AU-YOUNG, Janice
APPLICANT: YANG, Junming
APPLICANT: HARLAND, Lee
APPLICANT: WALSH, Roderick T.
APPLICANT: IO, Terence P.
APPLICANT: BOROMSKY, Mark L.
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0044 PCT
CURRENT APPLICATION NUMBER: US/10/220.382
PRIORITY FILING DATE: 2001-03-01
PRIORITY APPLICATION NUMBERS: 60/186,854; 60/188,384; 60/190,453; 60/190,730
PRIORITY FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
NUMBER OF SEQ. ID NOS. 42
SOFTWARE: PERL Program
SEQ ID NO 4
LENGTH: 368
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 2289894CD1
US-10-220-382-4

```

```

Query Match      18.9%   Score 438.5   DB 6;   Length 368;
Best Local Similarity 31.8%   Pred. No.2.9e-28;
Matches 127; Conservative 55; Indels 71; Gaps 14;

QY  40 ASE---SVALFFMLLDLTAVAGNAANVAIVIKTKPALRKFFVFHFLCYLDLALATIMPL 96
    111 1-1      :::: : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Db	9	ASEVAGSLGILLAAVNEVEGALLGNGALLVVLRRPGRBDALTYLAHLCVVDULLAAASTMPL	68
Qy	97	AMLSSSAL-FDHAFGEVYACRLTYFLVSCVFYSALILTSVAINERYVVVYVHMRKEYRMT	1555
Db	69	GILAAAPPGGLGRVRLGRPAFCRAAREFLSALLPACTLGVAAIGLARLYLIVHPLRPGSRP	128
Qy	156	LGLVAASYLVGVWVKALMAASYPVLGVRSWEGASVPGCSLQMSHAYCOL-----F	208
Db	129	PVL---VLTAWAAGLGLGALSTL-----GPPAPPPA-----PARCSVLAGGLGPF	1727
Qy	209	VVFEVAVLEFLPLRLILIVVYCSMFVARVAAMQHGPVPTWMETPPRORESLSKSTWTS	268
Db	173	RPLMALLAFALPALLLLGATGIGTIVVARALRL-PRPRA--RGSRLRSDLSDSLSTL--	227
Qy	269	SGADPTTPHRTFEGGKAAYVLLAVGGOFLCWLDPYFSFHLVVALSAOPISTGOVESVYTW	328
Db	228	---PPLRPR-LPGKAKALAPALVAGFOACWLF-----GCACLAAPARAAEAEAVTW	277
Qy	329	IGYFCTSNPFYFGCLNNQIR---GELSKQVCCFKAPREBELRLPSREGSIEENLDQFL	385
Db	278	VAYSFAAHPRFLYGLQRPVLAIGRLSRRL-----GGPVR-----	314
Qy	386	QQTGCPSESWSRPLPSKPQEPVADFRIPOIAIEETSE	424
Db	315	---ACTPQAHNPRALLDCLQRPFGPAGVSPSEAPQIPE 350	

### RESULT 13

```

US-60-389-987-208
? Sequence 208. Application US/60389987
? GENERAL INFORMATION:
? APPLICANT: Ghosh, Soumitra S.
? APPLICANT: Fany, Eoin D.
? APPLICANT: Zhang, Bing
? APPLICANT: Gibson, Bradford W.
? APPLICANT: Taylor, Steven W.
? APPLICANT: Glenn, Gary M.
? APPLICANT: Warnock, Dale E.
? TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
? TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
? FILE REFERENCE: 660088.465P2
? CURRENT APPLICATION NUMBER: US/60/389,987
? CURRENT FILING DATE: 2002-06-17
? NUMBER OF SEQ ID NOS: 3025
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 208
? LENGTH: 348
? TYPE: prt
? ORGANISM: Homo sapiens
US-60-389-967-208

```

Query Match	15.0%	Score 347	DB 7	Length 348
Best Local	28.6%	Pred. No. 1.2e-20		
Matches 99	Conservative 57	Mismatches 132	Indels 58	Gaps 10

[illegible]

Db 229 ----ATVTLAAMGAFIICMPPEYFAFYRGLRGDDAINEMLEAIVLMGYANSALNPIL 284  
Oy 341 YGCLNROIRGELSKOFCFFKPAPEBELRPSREG---SIEENFLQ 383  
Db 285 YALNRPDRTGYOQLFCC-----RLANRSHKTSLSNASQ 320

## RESULT 14

US-60-412-418-208  
Sequence 208, Application US/60412418  
GENERAL INFORMATION:  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Fahy, Eoin D.  
APPLICANT: Zhang, Bing  
APPLICANT: Gibson, Bradford W.  
APPLICANT: Taylor, Steven W.  
APPLICANT: Glenn, Gary M.  
APPLICANT: Warnock, Dale E.  
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
FILE REFERENCE: 660088.465P3  
CURRENT APPLICATION NUMBER: US/60/412.418  
CURRENT FILING DATE: 2002-09-20  
NUMBER OF SEQ ID NOS: 3025  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 208  
LENGTH: 348  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-60-412-418-208

Query Match 15.0% Score 347; DB 7; Length 348;  
Best Local Similarity 28.6% Pred. No. 1.2e-20;  
Matches 99; Conservative 57; Mismatches 132; Indels 58; Gaps 10;

Oy 49 MLLDLTAAGNAVMAYIAKTPALRKFEV--FVPHLCVLDLAALTMPLMLSSALFD 106  
Db 22 LAVILITVAGNVVCLAVGLNRRLNLTNCFIVSLATDILLGLVLPF-----SAIQ 76  
Oy 107 HAL---FGEVACRLYLPLSVCFVSLAIISSAIVNERYIVVHPKREYRMTGLVASVL 163  
Db 77 LSCWMSFGKVCNITYTSLDVMCLTASINLPMISLDRCAYMDPLRYVLTVPARVAISL 136  
Oy 164 VGWVWKALAMASVPY-LGRVSMEGAPS--VPGCCSLQMSHSAVCQLVVFVAVLYFLP 220  
Db 137 VLIWVISTTSLFSLHGMNSRNETSKGNHTTSKCNVYN-----EYGLVDGLVTFPLP 191  
Oy 221 LLLILVYCSMFYARVAAMQHGRLPTWMTTPRORSESLSSRSTWVTSSGAPQTPHRTF 280  
Db 192 LLINCIFYRIFRYARADQAKRIDHSSWK-----AATIREHR-- 228  
Oy 281 GGGAAVVLAVGOGFLCMLPIFFSFHLYVALSAQPISTGOVESVYTWIGYFCFTSNPFF 340  
Db 229 ---ATVTLAAMGAFIICMPPEYFAFYRGLRGDDAINEMLEAIVLMGYANSALNPIL 284  
Oy 341 YGCLNROIRGELSKOFCFFKPAPEBELRPSREG---SIEENFLQ 383  
Db 285 YALNRPDRTGYOQLFCC-----RLANRSHKTSLSNASQ 320

## RESULT 15

US-09-546-038A-31  
Sequence 31, Application US/09546038A  
GENERAL INFORMATION:  
APPLICANT: Gould-Rothberg, Bonnie  
TITLE OF INVENTION: METHOD OF IDENTIFYING LIGANDS FOR THE PEROXISOME  
TITLE OF INVENTION: PROLIFERATOR ACTIVATED RECEPTOR GAMMA USING  
TITLE OF INVENTION: DIFFERENTIAL GENE EXPRESSION  
FILE REFERENCE: 15966-549 METHOD OF IDENTIFYING LIGAND  
CURRENT APPLICATION NUMBER: US/09/546.038A  
CURRENT FILING DATE: 2000-04-10  
NUMBER OF SEQ ID NOS: 3025  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 31  
LENGTH: 400  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-09-546-038A-31

NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 31  
LENGTH: 400  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-09-546-038A-31

Query Match 14.5% Score 337; DB 5; Length 400;  
Best Local Similarity 28.2% Pred. No. 9.5e-20;  
Matches 120; Conservative 65; Mismatches 168; Indels 52; Gaps 17;

Oy 4 SPIPOSSGNSSTLGRVPO--TPGSPASGVPEUGKRDVASEVALFEMLLDUTAVAGNAA 62  
Db 2 APWPKNGSLAFWSDAPLDPSAANTSGLPVY-----PMAALAGALLALATVGGHLL 54  
Oy 63 VMAVIATKTPALRKF--VFPHLCVLDLAALTMPLMLSSALFDHALFGEVACRLYLF 120  
Db 55 VITAIARTPRLOTTITNVEVTSLATADLVGLVMPG--ATLALIGHMPLGATGCELMTS 112  
Oy 121 LSVCFVSLAIISSAIVNERYIVVHPKREYRMTGLVASVLYGVWVKALAMASVPVLG 180  
Db 113 VDVLCVTASITLGLALAVDRYLAVTNPLRYGTLYTKRRARAAYVLMVTSATVSFAPIMS 172  
Oy 181 RVSMEGAPSVPPGCCSLQMSHSAVCQL-----FVVVFVAVLYFLPLLLILVYCSMPRYA 235  
Db 173 Q-WNRVGADAEAOECH---SNPRCCSFASNMPTALLSSVSFYLPLVLMLEFVARVAVYA 228  
Oy 236 ---RVAAMQHGRLPTWMTTPR--ORSESLSSRSTWVTSSGAPQ--TTPHR--TFGGGKA 285  
Db 229 KRORRLRRELGRPPP--EESPRSPSRSPSPATVGTPTASDGVPSGRRPARLPLGEMRA 287  
Oy 286 AVVLLAVGOGFLCMLPIFFSFHLYVALSAQPISTGOVESVYTWIGYFCFTSNPFFYGLN 345  
Db 288 LRTGLIMGIFSLCMLPFFFLANVLAIVGSLVPSGVITALNMWLGANSANFPLLY-CRS 346  
Oy 346 ROIRGELSKOFCFFKPAPEBELR-----LPSREGSIEENFLQIQTGCGPSESWSVS 397  
Db 347 PDFR-DARRLICSYGGNGPEEPYVTPPASPVASRONSPLNRF-----DGYEGE---- 395  
Oy 398 RPLPS 402  
Db 396 RPPPT 400

Search completed: October 21, 2002, 16:13:37  
Job time : 47 secs

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PF 29-MAR-2001: 2001WO-US10436.  
XX  
XX 29-MAR-2000: 2000US-193051P.  
PR 06-APR-2000: 2000US-195155P.  
PR 20-APR-2000: 2000US-199084P.  
PR 28-APR-2000: 2000US-200551P.  
PR 05-MAY-2000: 2000US-202278P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX  
PI Policky JL, Tribouley CM, Tang YT, Baughn MR, Graul R, Khan FA,  
PI Nguyen DB, Patterson C, Lai P, Au-young J, Yang J, Hafalia A;  
PI Walla NK, Das D;  
XX  
XX WPI: 2001-616472/71.  
DR N-PSDB: AAD19579.  
XX  
XX New human G-protein coupled receptors, useful for treatment and  
PT diagnosis of e.g. cell proliferation, also screening for specific  
PT modulators, and related nucleic acid  
XX  
XX  
PS Claim 1: Page 104-105; 111pp; English.  
XX  
XX The present sequence is a human G-protein coupled receptor, GCRC-3  
CC protein. The GCRCs are used for treating or preventing disorders  
CC associated with decreased expression of functional GCRC, and for  
CC identifying specific agonists and antagonists, also binding agents  
CC and modulators. They can also be used for generating specific antibodies  
CC and for proteosome analysis. Disorders that can be treated include  
CC cell proliferative disorders, e.g., arteriosclerosis and cancer,  
CC neurological disorders, e.g., Huntington's disease and Parkinson's  
CC disease, cardiovascular disorders, e.g., atherosclerosis and congestive  
CC heart failure, gastrointestinal disorders, e.g., gastritis and nausea,  
CC autoimmune/inflammatory disorders, e.g., acquired immunodeficiency  
CC syndrome (AIDS) and anaemia, metabolic disorders, e.g., diabetes and  
CC obesity and viral infections. Nucleic acids that encode GCRC are  
CC used for identifying agents that alter its expression, for assessing  
CC toxicity of test compounds, and as sources of primers and probes for  
CC diagnostic detection of GCRC DNA and of therapeutic antisense and  
CC ribozyme sequences. They can also be used in gene therapy, for  
CC chromosomal mapping, and for recombinant production of GCRC. The  
CC antibodies are useful for diagnosis and monitoring of diseases  
CC associated with GCRC expression, for detecting and purifying GCRC,  
CC and as therapeutic agents and for drug screening.  
XX  
XX  
SQ Sequence 451 AA:  
  
Query Match 100.0% Score 2318: DB 22: Length 451:  
Best Local Similarity 100.0% Pred. No. 2e-228:  
Matches 451: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
  
OY 1 MESSPIPOSSGNSSTLGRVPTGPGSTAGVPEVGLRDVASEVALFLLDLDTVAAGN 60  
DB 1 MESSPIPOSSGNSSTLGRVPTGPGSTAGVPEVGLRDVASEVALFLLDLDTVAAGN 60  
OY 61 AAVMAVIAKTPALRKRFVFFHCLVDLLAALTLMLAMLSALLDEHALFGEVACRLYL 120  
DB 61 AAVMAVIAKTPALRKRFVFFHCLVDLLAALTLMLAMLSALLDEHALFGEVACRLYL 120  
OY 121 LSVCFVSLAIISSVAIINVERYYVHPMRVEYRMTGLTAVSLGVWVYALMASVPVIG 180  
DB 121 LSVCFVSLAIISSVAIINVERYYVHPMRVEYRMTGLTAVSLGVWVYALMASVPVIG 180  
OY 181 RVSWEAGAPSPVPGCSLQWSHSAACLFVYFAVLVFLPLLLIIVVYCSMFRVARVAM 240  
DB 181 RVSWEAGAPSPVPGCSLQWSHSAACLFVYFAVLVFLPLLLIIVVYCSMFRVARVAM 240  
OY 241 OHGRLPTWMEFPRORSESSSRSTVNTSSGAPQTPPHRTGGGKAAYVLAVGGFLLCW 300  
DB 241 OHGRLPTWMEFPRORSESSSRSTVNTSSGAPQTPPHRTGGGKAAYVLAVGGFLLCW 300  
OY 301 LPYFSFHLVVALSADPISITGVESVVTWIGYFCFTSNPFYGLNRQINGELSKQFVCF 360  
DB 301 LPYFSFHLVVALSADPISITGVESVVTWIGYFCFTSNPFYGLNRQINGELSKQFVCF 360

DB 301 LPYFSFHLVVALSADPISITGVESVVTWIGYFCFTSNPFYGLNRQINGELSKQFVCF 360  
OY 361 KPAPHEELRLPREGSIEENFLQGTGCPSESWSRPLSPKOPPAVDRIPOQIAE 420  
DB 361 KPAPHEELRLPREGSIEENFLQGTGCPSESWSRPLSPKOPPAVDRIPOQIAE 420  
OY 421 ETSEFLEQQLTSDIIMSUSYLRPAASPRLES 451  
DB 421 ETSEFLEQQLTSDIIMSUSYLRPAASPRLES 451  
  
RESULT 2  
AAU07900  
ID AAU07900 standard; Protein: 451 AA.  
XX  
XX AAU07900;  
AC  
XX  
XX 18-DEC-2001 (first entry)  
DT  
XX  
XX Human serotonin-like G protein-coupled receptor (5-HT-GPCR).  
DE  
XX  
XX Human, serotonin-like G protein-coupled receptor; 5-HT-GPCR;  
KW peripheral nervous system; central nervous system; PNS; CNS;  
KW brain injury; mood disorder; anxiety disorder; sleep disorder;  
KW neurogenic; myopathic disorder; neurodegenerative disorder;  
KW tranquilizer; nootropic; neuroprotective; antiparkinsonian;  
KW analgesic; cerebroprotective.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200170967-A2.  
PN  
XX  
XX 27-SEP-2001.  
PD  
XX  
XX 19-MAR-2001; 2001WO-EP03117.  
PE  
XX  
XX 20-MAR-2000; 2000US-190104P.  
PR 12-JUN-2000; 2000US-210975P.  
PR 14-DEC-2000; 2000US-255110P.  
XX  
XX (FARB ) BAYER AG.  
PA  
XX  
XX Ramakrishnan S;  
PI  
XX  
XX N-PSDB: AAS12583.  
DR  
XX  
XX New polynucleotide encoding a polypeptide which regulates, prevents and  
PT treats diseases of the peripheral or central nervous system including  
PT Alzheimer's Disease, comprises the human serotonin-like G  
PT protein-coupled receptor polynucleotide  
XX  
XX  
PS Claim 1: Fig 2; 88pp; English.  
  
The present invention relates to the isolation of a novel DNA sequence  
CC encoding a human serotonin-like G protein-coupled receptor (5-HT-GPCR)  
CC polypeptide. The sequences of the invention are useful for screening for  
CC agents which decrease the activity of 5-HT-GPCR or for identifying agents  
CC which regulate the activity of 5-HT-GPCR. A reagent that modulates the  
CC activity of 5-HT-GPCR is useful for detecting 5-HT-GPCR in a biological  
CC sample and for reducing the activity of 5-HT-GPCR in a cell. A  
CC pharmaceutical composition comprising such a reagent is useful for  
CC preventing or ameliorating disorders of the peripheral or central nervous  
CC system, preferably primary or secondary disorders after brain injury,  
CC mood disorders, anxiety disorders, disorders of thought and volition,  
CC sleep disorders, diseases of the motor unit such as neurogenic and  
CC myopathic disorders, neurodegenerative disorders (e.g. Alzheimer's  
CC disease, Parkinson's disease) or disorders leading to peripheral and  
CC chronic pain. The coding sequence of 5-HT-GPCR polynucleotide is useful  
CC for generating antisense oligonucleotides or ribozymes which specifically  
CC bind to mRNA transcribed from the 5-HT-GPCR polynucleotide. These  
CC antisense oligonucleotides are useful for modulating 5-HT-GPCR gene  
CC expression. Polynucleotide sequences encoding for 5-HT-GPCR may be used



CC In gene therapy. The present sequence represents the novel human  
 CC 5-HT-GPCR polypeptide of the invention.

XX Sequence 451 AA:

Query Match 100.0%; Score 2318; DB 22; Length 451;

Best Local Similarity 100.0%; Pred. No. 2e-228;

Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTLGRVPTGPSTAGVPEVGLRDVASSVALFFMLLDLTVAVGN 60  
 DB 1 MESSPIPOSSGNSSTLGRVPTGPSTAGVPEVGLRDVASSVALFFMLLDLTVAVGN 60  
 QY 61 AAVMAVIATPALRKVFVFHCLVDLLAATLPLAMLSSALFPHALFGEVACRLTYF 120  
 DB 61 AAVMAVIATPALRKVFVFHCLVDLLAATLPLAMLSSALFPHALFGEVACRLTYF 120  
 QY 121 LSVCFVSLAITSVAINVERYYVHPMRYEVRMTGLVASVLYGVWVAKALMAASVPVLG 180  
 DB 121 LSVCFVSLAITSVAINVERYYVHPMRYEVRMTGLVASVLYGVWVAKALMAASVPVLG 180  
 QY 181 RVSMEGAPSVPPGCSLQMSHSAYCOLFVYVAVLYFLLPLLLIIVYCSMRVARVAA 240  
 DB 181 RVSMEGAPSVPPGCSLQMSHSAYCOLFVYVAVLYFLLPLLLIIVYCSMRVARVAA 240  
 QY 241 OHGPLPTWMEPRORSESISSRTWTSSGAPQTPHRTFEGGKAAVLLAVGGOFLLCW 300  
 DB 241 OHGPLPTWMEPRORSESISSRTWTSSGAPQTPHRTFEGGKAAVLLAVGGOFLLCW 300  
 QY 301 LPYFSEHLVALSAOPISTGVESVVTWIGYFCFTSNPFYGCILNRQINGELSKQVCF 360  
 DB 301 LPYFSEHLVALSAOPISTGVESVVTWIGYFCFTSNPFYGCILNRQINGELSKQVCF 360  
 QY 361 KPAPEEELRLPSREGSIENFLQFLOGTCGPEBSWVSRPLPSKQEPVAVDRIPQIAE 420  
 DB 361 KPAPEEELRLPSREGSIENFLQFLOGTCGPEBSWVSRPLPSKQEPVAVDRIPQIAE 420  
 QY 421 ETSEFLDQUTSDIIMSDSYLRPAASPRLES 451  
 DB 421 ETSEFLDQUTSDIIMSDSYLRPAASPRLES 451

# RESULT 3

AAU08710 standard; Protein: 451 AA.

AC AAU08710;

XX 18-DEC-2001 (first entry)

DE Human histamine H2-like G protein-coupled receptor polypeptide.

XX Histamine H2-like G protein-coupled receptor; histamine H2-like GPCR;  
 KW digestive system; immune system; respiratory system; reproductive system;  
 KW urinary system; peripheral nervous system; central nervous system; human;  
 KW brain injury; mood disorder; anxiety; thought disorder; sleep disorder;  
 KW motor unit disease; neurogenic disorder; myopathic disorder; neuroleptic;  
 KW neurodegenerative disorder; psychotic disorder; cerebrovascular disorder;  
 KW Alzheimer's disease; Parkinson's disease; muscle spasm; peripheral pain;  
 KW chronic pain; tranquilizer; nootropic; neuroprotective; antiparkinsonian;  
 KW analgesic; antidepressant; antiallergic; antiinflammatory; gene therapy;  
 KW cerebroprotective; vulnerary.

OS Homo sapiens.

PN WO200170812-A2.

PD 27-SEP-2001.

PF 20-MAR-2001; 2001WO-EP03162.

PR 20-MAR-2000; 2000US-190554P.  
 12-JUN-2000; 2000US-210734P.

PR 14-DEC-2000; 2000US-255147P.

XX (FARB ) BAYER AG.

XX Ramakrishnan S;

DR WPI: 2001-611486/70.

DR N-PSDB: AAS14725.

PT New human histamine H2-like G protein-coupled receptor polynucleotide  
 PT and polypeptide which can be regulated for preventing, treating  
 PT diseases of digestive, immune, respiratory, reproductive or central  
 PT nervous system -

PS Claim 1: Fig 2: 93pp: English.

XX The invention relates to a human histamine H2-like G protein-coupled  
 CC receptor (GPCR) polypeptides and the nucleic acids encoding them. The  
 CC sequences are useful for screening for agents which regulate the activity  
 CC of histamine H2-like GPCR by contacting test compounds with the  
 CC polypeptide and monitoring the activity. The polypeptides and their  
 CC associated DNA sequences are useful for modulating the activity of a  
 CC histamine H2-like GPCR in a disease of the digestive, immune,  
 CC respiratory, reproductive, urinary, peripheral or central nervous system,  
 CC especially a primary or secondary disorder after brain injury, disorder  
 CC of mood, an anxiety disorder, a disorder of thought, a disorder of sleep,  
 CC a disease of the motor unit, a neurogenic and myopathic disorder, a  
 CC neurodegenerative disorder, a psychotic disorder, a cerebrovascular  
 CC disorder, Alzheimer's disease, Parkinson's disease, muscle spasms or a  
 CC disorder leading to peripheral and chronic pain. This sequence represents  
 a human histamine H2-like GPCR polypeptide.

SQ Sequence 451 AA:

Query Match 100.0%; Score 2318; DB 22; Length 451;

Best Local Similarity 100.0%; Pred. No. 2e-228;

Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTLGRVPTGPSTAGVPEVGLRDVASSVALFFMLLDLTVAVGN 60  
 DB 1 MESSPIPOSSGNSSTLGRVPTGPSTAGVPEVGLRDVASSVALFFMLLDLTVAVGN 60  
 QY 61 AAVMAVIATPALRKVFVFHCLVDLLAATLPLAMLSSALFPHALFGEVACRLTYF 120  
 DB 61 AAVMAVIATPALRKVFVFHCLVDLLAATLPLAMLSSALFPHALFGEVACRLTYF 120  
 QY 121 LSVCFVSLAITSVAINVERYYVHPMRYEVRMTGLVASVLYGVWVAKALMAASVPVLG 180  
 DB 121 LSVCFVSLAITSVAINVERYYVHPMRYEVRMTGLVASVLYGVWVAKALMAASVPVLG 180  
 QY 181 RVSMEGAPSVPPGCSLQMSHSAYCOLFVYVAVLYFLLPLLLIIVYCSMRVARVAA 240  
 DB 181 RVSMEGAPSVPPGCSLQMSHSAYCOLFVYVAVLYFLLPLLLIIVYCSMRVARVAA 240  
 QY 241 OHGPLPTWMEPRORSESISSRTWTSSGAPQTPHRTFEGGKAAVLLAVGGOFLLCW 300  
 DB 241 OHGPLPTWMEPRORSESISSRTWTSSGAPQTPHRTFEGGKAAVLLAVGGOFLLCW 300  
 QY 301 LPYFSEHLVALSAOPISTGVESVVTWIGYFCFTSNPFYGCILNRQINGELSKQVCF 360  
 DB 301 LPYFSEHLVALSAOPISTGVESVVTWIGYFCFTSNPFYGCILNRQINGELSKQVCF 360  
 QY 361 KPAPEEELRLPSREGSIENFLQFLOGTCGPEBSWVSRPLPSKQEPVAVDRIPQIAE 420  
 DB 361 KPAPEEELRLPSREGSIENFLQFLOGTCGPEBSWVSRPLPSKQEPVAVDRIPQIAE 420  
 QY 421 ETSEFLDQUTSDIIMSDSYLRPAASPRLES 451  
 DB 421 ETSEFLDQUTSDIIMSDSYLRPAASPRLES 451

# RESULT 4

AAU04367

ID AA004367 standard; Protein: 451 AA.  
XX  
AC AA004367;  
XX  
DT 23-OCT-2001 (first entry)  
XX  
DE Human G-protein coupled receptor, hRUP13.  
XX  
KW Human; G-protein coupled receptor; GPCR; hRUP13; agonist;  
XX Inverse agonist; Lung Cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200136471-A2.  
XX  
PD 25-MAY-2001.  
XX  
PE 16-NOV-2000; 2000WO-US31509.  
XX  
PR 17-NOV-1999; 99US-0166088.  
PR 17-NOV-1999; 99US-0166099.  
PR 17-NOV-1999; 99US-0166369.  
PR 23-DEC-1999; 99US-0171900.  
PR 23-DEC-1999; 99US-0171901.  
PR 23-DEC-1999; 99US-0171902.  
PR 11-FEB-2000; 2000US-0181749.  
PR 14-MAR-2000; 2000US-0189258.  
PR 10-APR-2000; 2000US-0189259.  
PR 10-APR-2000; 2000US-0195898.  
PR 10-APR-2000; 2000US-0195899.  
PR 10-APR-2000; 2000US-0196078.  
PR 28-APR-2000; 2000US-0200419.  
PR 12-MAY-2000; 2000US-0203630.  
PR 12-JUN-2000; 2000US-0210741.  
PR 12-JUN-2000; 2000US-0210982.  
PR 21-AUG-2000; 2000US-0226760.  
PR 26-SEP-2000; 2000US-0235418.  
PR 26-SEP-2000; 2000US-0235779.  
PR 20-OCT-2000; 2000US-0242332.  
PR 20-OCT-2000; 2000US-0242343.  
XX  
XX (AREN-) ARENA PHARM INC.  
XX  
PI Chen R, Dang HT, Lowitz KP;  
XX  
DR MPI: 2001-355616/37.  
DR N-PSDB: AAS07940.  
XX  
XX Endogenous and non-endogenous versions of human G-protein coupled  
PT receptors for direct identification of candidate compounds as agonists,  
PT Inverse agonists or partial agonists for use as therapeutic agents -  
XX  
PS Claim 21; Page 98-100; 160pp; English.  
XX  
XX The sequence represents a human G-protein coupled receptor (GPCR),  
CC hRUP13. The endogenous and non-endogenous, constitutively activated  
CC versions of human G-protein coupled receptors (GPCR), are useful for  
CC direct identification of candidate compounds as receptor agonists,  
CC Inverse agonists or partial agonists having applicability as therapeutic  
CC agents for treating diseases related to GPCR, e.g. lung cancer.  
CC Non-endogenous version of human GPCRs are also utilized in research  
CC settings and in vitro and in vivo system, incorporating GPCRs can be  
CC utilized to elucidate and understand the roles these receptors  
CC play in the human condition, both normal and diseased.  
CC  
XX  
SO Sequence 451 AA:  
  
Query Match 100.0%; Score 2318; DB 22; Length 451;  
Best Local Similarity 100.0%; Pred. No. 2e-228;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MESSPIPOSSGNSSTLGRVPOTPGPSTASGVPEVGLRDVASVVALFFMLLDLTAVAGN 60  
XX

Db 1 MESSPIPOSSGNSSTLGRVPOTPGPSTASGVPEVGLRDVASVVALFFMLLDLTAVAGN 60  
QY 61 AAVMAVIAKTPALRKREVFVFHLCVLDLALTLMPALMLSSALFPDHALFGVACRLYLEF 120  
XX  
Db 61 AAVMAVIAKTPALRKREVFVFHLCVLDLALTLMPALMLSSALFPDHALFGVACRLYLEF 120  
QY 121 LSVCFVSLAILSVSAINVERYYYYVHPMRVEYRMTLGLVASVYGVWVKALAMASVPLVG 180  
XX  
Db 121 LSVCFVSLAILSVSAINVERYYYYVHPMRVEYRMTLGLVASVYGVWVKALAMASVPLVG 180  
QY 181 RVSMEGAPSVPPGCSLQMSHSAYCQLFVVVFAVLYFLPLLLLVVYCSMFRARVAAM 240  
XX  
Db 181 RVSMEGAPSVPPGCSLQMSHSAYCQLFVVVFAVLYFLPLLLLVVYCSMFRARVAAM 240  
QY 241 OHGPLPTWMTETPROSESLSRSTWTSAGAPOTTPHRTFGGKAAYVLLVAVGGOFLLCW 300  
XX  
Db 241 OHGPLPTWMTETPROSESLSRSTWTSAGAPOTTPHRTFGGKAAYVLLVAVGGOFLLCW 300  
QY 301 LPYFSFHLVYALSAOPISTGQVESVVTWIGYFCFTSNPFYGCILNRQIRGELSKQVCFE 360  
XX  
Db 301 LPYFSFHLVYALSAOPISTGQVESVVTWIGYFCFTSNPFYGCILNRQIRGELSKQVCFE 360  
QY 361 KPAPPEELRLPSREGSIEENFLQGTGCPSESWSRPLSPKQEPAPVDFRIPGQIAE 420  
XX  
Db 361 KPAPPEELRLPSREGSIEENFLQGTGCPSESWSRPLSPKQEPAPVDFRIPGQIAE 420  
QY 421 ETSEFLQQLTSDIIMSDSLRLPASPRLLES 451  
XX  
Db 421 ETSEFLQQLTSDIIMSDSLRLPASPRLLES 451  
  
RESULT 5  
AAG64123  
ID AAG64123 standard; Protein: 451 AA.  
XX  
AC AAG64123;  
XX  
DT 25-SEP-2001 (first entry)  
XX  
XX  
DE Human G protein-coupled receptor GPRV47.  
XX  
XX  
KW Human; guanosine triphosphate binding protein-coupled receptor;  
KW G protein-coupled receptor; GPRV8; GPRV12; GPRV16; GPRV21; GPRV40;  
KW GPRV47; GPRV51; GPRV71; GPRV72; Cancer; Liver cirrhosis;  
KW Alzheimer's disease; cytosstatic; hepatocytic; nootropic;  
KW neuroprotective; gene therapy; peptide therapy.  
XX  
XX  
OS Homo sapiens.  
XX  
PN WO200148188-A1.  
XX  
PD 05-JUL-2001.  
XX  
PE 28-DEC-2000; 2000WO-JP09408.  
XX  
PR 28-DEC-1999; 99JP-0375152.  
PR 31-MAR-2000; 2000JP-0101339.  
XX  
PA (HELI-) HELIX RES INST.  
XX  
PI Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;  
PI Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;  
XX  
DR MPI: 2001-425662/45.  
DR N-PSDB: AAH73514.  
XX  
XX  
XX New DNA encoding guanosine triphosphate binding protein coupled  
PT receptors and their expression products for screening potential  
PT anticancer and nootropic drugs and in diagnosis of these diseases -  
XX  
PS Example 1; Page 126-129; 170pp; Japanese.  
XX  
CC The invention relates to nine human guanosine triphosphate binding

CC protein (G protein)-coupled receptors designated GPRv8, GPRv12, GPRv16, GPRv21, GPRv40, GPRv47, GPRv51, GPRv71 and GPRv72, and to the CC genes encoding them. These genes and proteins and antibodies against CC the protein are useful in the treatment, prevention, diagnosis and CC investigation of diseases associated with G protein-coupled receptors, CC including cancer, cirrhosis of the liver and Alzheimer's disease. CC The present sequence is a G protein-coupled receptor of the invention. CC  
XX Sequence 451 AA:  
SQ  
Query Match 100.0%; Score 2318; DB 22; Length 451;  
Best Local Similarity 100.0%; Pred. No. 2e-228;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MESSPIPOSSGNSSITLGRVPTGPSTASGYPEVGLRDVASESVALFFMLLDITAVAGN 60  
Db 1 MESSPIPOSSGNSSITLGRVPTGPSTASGYPEVGLRDVASESVALFFMLLDITAVAGN 60  
QY 61 AAVMAVIKTPALRKRFVVFHLCVLDLALTLPLMLSSALFDHALFGEVACRLYLF 120  
Db 61 AAVMAVIKTPALRKRFVVFHLCVLDLALTLPLMLSSALFDHALFGEVACRLYLF 120  
QY 121 LSVCFVSLAITSVAINVERYYYVHPMRXEVRMTLGLVASVLGVWVKALAMASVPLG 180  
Db 121 LSVCFVSLAITSVAINVERYYYVHPMRXEVRMTLGLVASVLGVWVKALAMASVPLG 180  
QY 181 RVSNEEGAPSVPPGCSLQMSHSAVCQLFVVFAVLYFLPLLLLVVCSMFRARVAAM 240  
Db 181 RVSNEEGAPSVPPGCSLQMSHSAVCQLFVVFAVLYFLPLLLLVVCSMFRARVAAM 240  
QY 241 OHGPLPTMETPRORSESLSRSTMTSSGAPOTTPHRTFGGKAAVLLAVGGOFLLCW 300  
Db 241 OHGPLPTMETPRORSESLSRSTMTSSGAPOTTPHRTFGGKAAVLLAVGGOFLLCW 300  
QY 301 LPYFSFHLVYALSAQPISTGVESVWTWIGYFCFTSNPFYGCUNROI RIGELSKQVCF 360  
Db 301 LPYFSFHLVYALSAQPISTGVESVWTWIGYFCFTSNPFYGCUNROI RIGELSKQVCF 360  
QY 361 KPAPEELRLRSRGSTIENFLQIQTGCGSESVSRPLSPKOEPAVDFRIPGOIAE 420  
Db 361 KPAPEELRLRSRGSTIENFLQIQTGCGSESVSRPLSPKOEPAVDFRIPGOIAE 420  
QY 421 ETSEFLEQOLTSDIIMSDSYLRPAASPRLES 451  
Db 421 ETSEFLEQOLTSDIIMSDSYLRPAASPRLES 451  
RESULT 6  
AAU04386  
ID AAU04386 standard; Protein: 869 AA.  
XX  
AC AAU04386;  
XX  
DT 23-OCT-2001 (first entry)  
XX  
DE GPCR-Gs fusion protein, hRUP13-GS.  
XX  
KW G-protein coupled receptor; GPCR; hRUP13-Gs; agonist;  
XX  
XX Inverse agonist; lung cancer.  
XX  
OS Chimeric - Homo sapiens.  
XX  
XX Chimeric - Rattus sp.  
XX  
XX WO200136471-A2.  
XX  
XX  
XX 25-MAY-2001.  
XX  
XX 16-NOV-2000; 2000WO-US31509.  
XX  
XX 17-NOV-1999; 99US-0166088.  
XX 17-NOV-1999; 99US-0166099.  
XX 17-NOV-1999; 99US-0166369.  
XX 23-DEC-1999; 99US-0171900.

PR 23-DEC-1999; 99US-0171901.  
PR 23-DEC-1999; 99US-0171902.  
PR 11-FEB-2000; 2000US-0181749.  
PR 14-MAR-2000; 2000US-0189258.  
PR 14-MAR-2000; 2000US-0189259.  
PR 10-APR-2000; 2000US-0195898.  
PR 10-APR-2000; 2000US-0195899.  
PR 10-APR-2000; 2000US-0196078.  
PR 28-APR-2000; 2000US-0200419.  
PR 12-MAY-2000; 2000US-0203630.  
PR 12-JUN-2000; 2000US-0210741.  
PR 12-JUN-2000; 2000US-0210982.  
PR 21-AUG-2000; 2000US-0226760.  
PR 26-SEP-2000; 2000US-0235418.  
PR 26-SEP-2000; 2000US-0235779.  
PR 20-OCT-2000; 2000US-0242332.  
PR 20-OCT-2000; 2000US-0242343.  
XX  
XX (AREN-) ARENA PHARM INC.  
XX  
XX Chen R, Dang HT, Lowitz KP;  
XX  
XX WPI: 2001-355616/37.  
XX N-PSDB: AAS08271.  
XX  
XX Endogenous and non-endogenous versions of human G-protein coupled  
XX receptors for direct identification of candidate compounds as agonists,  
XX inverse agonists or partial agonists for use as therapeutic agents -  
XX  
XX Example 5; Page 146-149; 160pp; English.  
XX  
XX The sequence is a G-protein coupled receptor (GPCR) fusion protein,  
XX hRUP13-Gs, being the human hRUP13 fused to the rat Gs protein.  
XX The endogenous and non-endogenous, constitutively activated versions  
XX of human G-protein coupled receptors (GPCR), are useful for direct  
XX identification of candidate compounds as receptor agonists, inverse  
XX agonists or partial agonists having applicability as therapeutic  
XX agents for treating diseases related to GPCR, e.g. lung cancer.  
XX Non-endogenous version of human GPCRs are also utilized in research  
XX settings and in vitro and in vivo system, incorporating GPCRs can be  
XX utilized to elucidate and understand the roles these receptors  
XX play in the human condition, both normal and diseased.  
XX  
SQ Sequence 869 AA:  
Query Match 100.0%; Score 2318; DB 22; Length 869;  
Best Local Similarity 100.0%; Pred. No. 5e-228;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MESSPIPOSSGNSSITLGRVPTGPSTASGYPEVGLRDVASESVALFFMLLDITAVAGN 60  
Db 1 MESSPIPOSSGNSSITLGRVPTGPSTASGYPEVGLRDVASESVALFFMLLDITAVAGN 60  
QY 61 AAVMAVIKTPALRKRFVVFHLCVLDLALTLPLMLSSALFDHALFGEVACRLYLF 120  
Db 61 AAVMAVIKTPALRKRFVVFHLCVLDLALTLPLMLSSALFDHALFGEVACRLYLF 120  
QY 121 LSVCFVSLAITSVAINVERYYYVHPMRXEVRMTLGLVASVLGVWVKALAMASVPLG 180  
Db 121 LSVCFVSLAITSVAINVERYYYVHPMRXEVRMTLGLVASVLGVWVKALAMASVPLG 180  
QY 181 RVSNEEGAPSVPPGCSLQMSHSAVCQLFVVFAVLYFLPLLLLVVCSMFRARVAAM 240  
Db 181 RVSNEEGAPSVPPGCSLQMSHSAVCQLFVVFAVLYFLPLLLLVVCSMFRARVAAM 240  
QY 241 OHGPLPTMETPRORSESLSRSTMTSSGAPOTTPHRTFGGKAAVLLAVGGOFLLCW 300  
Db 241 OHGPLPTMETPRORSESLSRSTMTSSGAPOTTPHRTFGGKAAVLLAVGGOFLLCW 300  
QY 301 LPYFSFHLVYALSAQPISTGVESVWTWIGYFCFTSNPFYGCUNROI RIGELSKQVCF 360  
Db 301 LPYFSFHLVYALSAQPISTGVESVWTWIGYFCFTSNPFYGCUNROI RIGELSKQVCF 360

QY 361 KPAPEEELRLPREGSIEENFLQGTGCPSESWSRPLPSKOEPPAVDFRIPGOIAE 420  
 |||||||  
 Db 361 KPAPEEELRLPREGSIEENFLQGTGCPSESWSRPLPSKOEPPAVDFRIPGOIAE 420  
 QY 421 ETSEFLQQLTSDIIMSDSYLRPASPRLES 451  
 |||||||  
 Db 421 ETSEFLQQLTSDIIMSDSYLRPASPRLES 451

## RESULT 7

AAU04382

ID AAU04382 standard; Protein: 451 AA.

AC AAU04382;

DT 23-OCT-2001 (first entry)

DE Human G-protein coupled receptor, hRUP13, mutant A268K.

XX Human; G-protein coupled receptor; GPCR; hRUP13; agonist;

KM Inverse agonist; lung cancer; A268K; mutant; mutein.

XX Homo sapiens.

OS WO200136471-A2.

PN 25-MAY-2001.

PD 16-NOV-2000; 2000MO-US31509.

PF 17-NOV-1999; 99US-0166088.

PR 17-NOV-1999; 99US-0166099.

PR 17-NOV-1999; 99US-0166369.

PR 23-DEC-1999; 99US-0171900.

PR 23-DEC-1999; 99US-0171902.

PR 11-FEB-2000; 2000US-0181749.

PR 14-MAR-2000; 2000US-0189259.

PR 14-MAR-2000; 2000US-0189259.

PR 10-APR-2000; 2000US-0195899.

PR 10-APR-2000; 2000US-0195899.

PR 10-APR-2000; 2000US-0196078.

PR 28-APR-2000; 2000US-0200419.

PR 12-MAY-2000; 2000US-0203630.

PR 12-JUN-2000; 2000US-0210741.

PR 12-JUN-2000; 2000US-0210982.

PR 21-AUG-2000; 2000US-0226760.

PR 26-SEP-2000; 2000US-0235418.

PR 26-SEP-2000; 2000US-0235779.

PR 20-OCT-2000; 2000US-0242332.

PR 20-OCT-2000; 2000US-0242343.

XX (AREN-) ARENA PHARM INC.

XX Chen R, Dang HT, Lowitz KP;

XX WPI: 2001-355616/37.

XX N-PSDB; AAS07997.

CC utilised to elucidate and understand the roles these receptors  
 CC play in the human condition, both normal and diseased.  
 CC Note: The sequence is mutated at Ala 268 not at position 268. The  
 CC description of the mutation is a typographical error in the  
 CC specification.  
 CC  
 SQ Sequence 451 AA;  
 Query Match 99.8%; Score 2313; DB 22; Length 451;  
 Best Local Similarity 99.8%; Pred. No. 6,6e-228;  
 Matches 450; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MESSPIPOSSGNSSTLGRVDPGPSTASGVPEVGLRDVASESYALFPMLLDITAVAGN 60  
 |||||||  
 Db 1 MESSPIPOSSGNSSTLGRVDPGPSTASGVPEVGLRDVASESYALFPMLLDITAVAGN 60  
 QY 61 AAVMAVIKTPALRKFFVPHLCVLDLAATLMPPLMLSSALFDNALGCEVACRYLF 120  
 |||||||  
 Db 61 AAVMAVIKTPALRKFFVPHLCVLDLAATLMPPLMLSSALFDNALGCEVACRYLF 120  
 QY 121 LSYCFVSLAISVSAINVERYYVYVHPMRVEVRMTLGLVASVLYGVWVKALAMASVPLG 180  
 |||||||  
 Db 121 LSYCFVSLAISVSAINVERYYVYVHPMRVEVRMTLGLVASVLYGVWVKALAMASVPLG 180  
 QY 181 RVSWEGAPSVPGCSLQWHSAYCOLFVVFAVLYFLPLLILVYCSMFRVAVAA 240  
 |||||||  
 Db 181 RVSWEGAPSVPGCSLQWHSAYCOLFVVFAVLYFLPLLILVYCSMFRVAVAA 240  
 QY 241 OHGPLPTMMETPRORSLSRSMTVSSGAPOTTPHRTGCGKAAYVLLAVGOFLLCW 300  
 |||||||  
 Db 241 OHGPLPTMMETPRORSLSRSMTVSSGAPOTTPHRTGCGKAAYVLLAVGOFLLCW 300  
 QY 301 LPYFSFHLVYALSAQPISTGVESVVTWIGYFCFTSNPFYGCINROI RGEISKQVCF 360  
 |||||||  
 Db 301 LPYFSFHLVYALSAQPISTGVESVVTWIGYFCFTSNPFYGCINROI RGEISKQVCF 360  
 QY 361 KPAPEEELRLPREGSIEENFLQGTGCPSESWSRPLPSKOEPPAVDFRIPGOIAE 420  
 |||||||  
 Db 361 KPAPEEELRLPREGSIEENFLQGTGCPSESWSRPLPSKOEPPAVDFRIPGOIAE 420  
 QY 421 ETSEFLQQLTSDIIMSDSYLRPASPRLES 451  
 |||||||  
 Db 421 ETSEFLQQLTSDIIMSDSYLRPASPRLES 451

## RESULT 8

AAG66453

ID AAG66453 standard; Protein: 279 AA.

XX AAG66453;

XX 15-NOV-2001 (first entry)

DE Human G protein coupled receptor, BiogCR31.

XX Human; G protein coupled receptor; BiogCR31.

XX Homo sapiens.

XX CN1299824-A.

XX 20-JUN-2001.

XX 16-DEC-1999; 99CN-0124252.

XX 16-DEC-1999; 99CN-0124252.

XX (SHAN-) SHANGHAI SHENGYUAN GENE DEV CO LTD.

XX Mao Y, Xie Y;

XX WPI: 2001-523186/58.

XX N-PSDB; AAH75973.

```
XX New human coupling acceptor and its code sequence - NoAbstract
PT
XX
XX Claim 1; Page 16-17 (Disclosure); 22pp; Chinese.
PS
XX The present sequence is the protein sequence for a novel human G protein
CC coupled receptor, BiogPCR31.
CC
XX
XX Sequence 279 AA:
SQ
Query Match 63.5%; Score 1472; DB 22; Length 279;
Best Local Similarity 100.0%; Pred. No. 4.3e-142;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 173 MASPVLCGRVMEGAPVPGCSLQMSHSAVCOLEFVVVFAVLFLPLLLIIVVYCSMF 232
DB 1 MASPVLCGRVMEGAPVPGCSLQMSHSAVCOLEFVVVFAVLFLPLLLIIVVYCSMF 60
QY 233 RVARVAAMQHGRLPTWMTPRQSESLSSRSTMTVSSGAPQTPHRTFGGKAAYVLLAV 292
DB 61 RVARVAAMQHGRLPTWMTPRQSESLSSRSTMTVSSGAPQTPHRTFGGKAAYVLLAV 120
QY 293 GGQFLCWLPIFSFHLVYALSAQPISTGOVESVVTWIGYFCFTSNPFYGCINRQIRGEL 352
DB 121 GGQFLCWLPIFSFHLVYALSAQPISTGOVESVVTWIGYFCFTSNPFYGCINRQIRGEL 180
QY 353 SKQFYCFKRPAPBEELRLPSREGSTEENFLQFLOGTGCPSRWRSRLPSPKQEPAYDF 412
DB 181 SKQFYCFKRPAPBEELRLPSREGSTEENFLQFLOGTGCPSRWRSRLPSPKQEPAYDF 240
QY 413 RIGQIAETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451
DB 241 RIGQIAETSEFLEQQLTSDIIMSDSYLRPAASPRLES 279
RESULT 9
AAW06595
ID AAW06595 standard; Protein; 252 AA.
XX
XX AAW06595;
AC
XX 17-FEB-1997 (first entry)
DT
XX
XX G protein conjugate receptor protein.
DE
XX
XX G protein conjugate receptor protein; rabbit; amplify;
KW stomach pylorus region smooth muscle cell; primer; PCR.
XX
XX Oryctolagus cuniculus.
OS
XX
XX JP08245697-A.
PN
XX
XX 24-SEP-1996.
PD
XX
XX 16-MAR-1995; 95JP-0057187.
PF
XX
XX 16-MAR-1995; 95JP-0057187.
PR
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX
XX WPI; 1996-482257/48.
DR
XX
XX N-PSDB; AAT49309.
PT
XX
XX New G protein conjugate receptor protein and related DNA - useful
PT for screening for drugs to inhibit G protein-ligand binding
XX
XX Claim 1; Fig 1 and 2; 25pp; Japanese.
PS
XX
XX This sequence represents a G protein conjugate receptor protein. The
CC cDNA encoding this sequence was purified from rabbit stomach pylorus
CC region smooth muscle cells using the primer sequences given in AAT49310-
CC 11. The G protein conjugate receptor protein may be used in the
CC development of new drugs.
```

```
XX
SQ Sequence 252 AA;
Query Match 55.0%; Score 1276; DB 17; Length 252;
Best Local Similarity 98.0%; Pred. No. 4.3e-122;
Matches 247; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 85 VDLAALFLMPLAMSSSALFDHALFGVACLYFLSVCFPSLAITSVAINVERYYV 144
DB 1 VDLAALFLMPLAMSSSALFDHALFGVACLYFLSVCFPSLAITSVAINVERYYV 60
QY 145 VHPMREYRMTLGLVASYLVGVWYKALAMASVPVLCGRVMEGAPVPGCSLQMSHSAV 204
DB 61 VHPMREYRMTLGLVASYLVGVWYKALAMASVPVLCGRVMEGAPVPGCSLQMSHSAV 120
QY 205 COLFVVFVAVLYFLPLLLIIVVYCSMFRVARVAAMQHGRLPTWMTPRQSESLSSRST 264
DB 121 COLFVVFVAVLYFLPLLLIIVVYCSMFRVARVAAMQHGRLPTWMTPRQSESLSSRST 180
QY 265 WYSSGAPQTPHRTFGGKAAYVLLAVGGQFLCWLPIFSFHLVYALSAQPISTGOVES 324
DB 181 WYSSGAPQTPHRTFGGKAAYVLLAVGGQFLCWLPIFSFHLVYALSAQPISTGOVES 240
QY 325 VWTWIGYFCFTS 336
DB 241 VWTWIGYFCFTS 252
RESULT 10
AAR91232
ID AAR91232 standard; Protein; 252 AA.
XX
XX AAR91232;
AC
XX 27-AUG-1996 (first entry)
DT
XX
XX Rabbit G-protein coupled receptor protein portion.
DE
XX
XX G-protein coupled receptor protein; G-PCR; agonist; antagonist;
KW cystic fibrosis; incontinence; diabetes; diagnosis; therapy.
XX
XX Oryctolagus cuniculus.
OS
XX
XX W09605302-A1.
PN
XX
XX 22-FEB-1996.
PD
XX
XX 10-AUG-1995; 95WO-JP01599.
PF
XX
XX 11-AUG-1994; 94JP-0189272.
PR
XX
XX 11-AUG-1994; 94JP-0189273.
PR
XX
XX 11-AUG-1994; 94JP-0189274.
PR
XX
XX 30-SEP-1994; 94JP-0236356.
PR
XX
XX 30-SEP-1994; 94JP-0236357.
PR
XX
XX 02-NOV-1994; 94JP-0270017.
PR
XX
XX 28-DEC-1994; 94JP-0326611.
PR
XX
XX 20-JAN-1995; 95JP-0007177.
PR
XX
XX 16-MAR-1995; 95JP-0057186.
PR
XX
XX 19-APR-1995; 95JP-0093989.
PA
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
PT
XX
XX Fuji R, Fukusumi S, Hinuma S, Hosoya M, Ohgi K;
PT Ohkaki T;
XX
XX WPI; 1996-139698/14.
DR
XX
XX N-PSDB; AAT13908.
PS
XX
XX G-protein coupled receptor protein DNA and protein - also methods
PT for isolating (ant)agonists for treatment of cystic fibrosis,
PT incontinence and diabetes
XX
XX Example 16; Page 263-64; 360pp; English.
```

XX A portion (AAR91232) of a novel rabbit gastropyloric part smooth  
CC muscle-derived G-protein coupled receptor protein (G-PCR) was  
CC identified as the product of cDNA clone PMN7 (AAR13908). The  
CC protein can be obtd. by expression of the encoding cDNA clone in  
CC transformed host cells. G-PCRs (see also AAR91217-25 and AAR91228-33)  
CC can be used to screen agonists and antagonists that modulate G-PCR  
CC activity, to raise antibodies and to develop assay systems.  
XX  
SQ Sequence 252 AA:  
Query Match 55.0%; Score 1276; DB 17; Length 252;  
Best Local Similarity 98.0%; Pred. No. 4.3e-122;  
Matches 247; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
OY 85 VDLALATLPLMLAMSSSALFDHALFGEVACRLYLFLSVCFYSLATLSVAINVERYYV 144  
DB 1 VDLALATLPLMLAMSSSALFDHALFGEVACRLYLFLSVCFYSLATLSVAINVERYYV 60  
OY 145 VHPMRREYRMTLGLVASVLYGVVKALAMASVPLGRVSWEGADSPGCSLQMSHAY 204  
DB 61 VHPMRREYRMTLGLVASVLYGVVKALAMASVPLGRVSWEGADSPGCSLQMSHAY 120  
OY 205 QCLEFVAVAVLYFLPLLLILVYCSMRVARVAMQGPPLTWMETRQRESLSNST 264  
DB 121 COLFVAVAVLYFLPLLLILVYCSMRVARVAMQGPPLTWMETRQRESLSNST 180  
OY 265 MYTSSGAPQTPHRTFEGGSKAAVLLAVGGPFLCMLPYFSPHLVVALSAOPISIGOVES 324  
DB 181 MYTSSGAPQTPHRTFEGGSKAAVLLAVGGPFLCMLPYFSPHLVVALSAOPISIGOVEN 240  
OY 325 VWTWIGYFCFTS 336  
DB 241 VWTWIGYFCFTS 252

RESULT 11  
AA005867  
ID AAO05867 standard; Protein: 138 AA.  
XX  
AC AAO05867;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 19759.  
XX  
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorders; arthritis; inflammation.  
XX  
OS Homo sapiens.  
XX  
PN WO200164835-A2.  
XX  
PD 07-SEP-2001.  
XX  
PF 26-FEB-2001; 2001WO-US04927.  
XX  
PR 28-FEB-2000; 2000US-0515126.  
XX  
PR 18-MAY-2000; 2000US-0377409.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Drmanac RT;  
XX  
DR WPI: 2001-514838/56.  
XX  
DR N-PSDB; AA185798.  
XX  
PT Isolated nucleic acids and polypeptides, useful for preventing  
PT diagnosing and treating e.g. leukaemia, inflammation and immune  
PT disorders -  
XX

PS Claim 20; SEQ ID NO 19759; 1399pp + Sequence listing; English.  
XX  
CC The invention relates to human polynucleotides (AA179941-AA193841) and  
CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, hematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pcl\_sequences.  
XX  
SQ Sequence 138 AA:  
Query Match 29.9%; Score 692; DB 22; Length 138;  
Best Local Similarity 97.7%; Pred. No. 1.2e-62;  
Matches 127; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
OY 272 POTTPTHTFEGGSKAAVLLAVGGPFLCMLPYFSPHLVVALSAOPISIGOVESVWTWIGY 331  
DB 1 POTTPTHTFEGGSKAAVLLAVGGPFLCMLPYFSPHLVVALSAOPISIGOVESVWTWIGY 60  
OY 332 PCFTSNPFYCGCLNQITGELSKOFCFCKPAPEBELRLPSREGSIENPFIQFLOGTGCP 391  
DB 61 PCFTSNPFYCGCLNQITGELSKOFCFCKPAPEBELRLPSREGSIENPFIQFLOGTGCP 120  
OY 392 SESWVSRLP 401  
DB 121 YKSWVSRLP 130

RESULT 12  
AAB19523  
ID AAB19523 standard; Protein: 368 AA.  
XX  
AC AAB19523;  
XX  
DT 09-JAN-2001 (first entry)  
XX  
DE G protein coupled receptor AXOR23.  
XX  
KW AXOR23; G protein coupled receptor; 7 transmembrane receptor;  
KW TM7 receptor; signal transduction; human; therapy;  
KW diagnosis; antibacterial; fungicide; protozoacide; viroicide;  
KW cytosolic; analgesic; antidiabetic; anorectic; antileptinemic;  
KW antiparkinsonian; hypotensive; hypertensive; osteopathic;  
KW antitumoral; cardiant; cerebroprotective; anticancer; antiallergic;  
KW antimigraine; antileptic; tranquilizer; neuroleptic; nootropic;  
KW anticonvulsant; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN WO200053622-A1.  
XX  
PD 14-SEP-2000.  
XX  
PF 01-MAR-2000; 2000WO-US05230.  
XX  
PR 09-MAR-1999; 99GB-0005317.  
XX  
PR 15-SEP-1999; 99US-0396610.  
XX  
PA (SMK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Elshourbagy N, Shabon U, Michalovich D;  
XX  
DR WPI: 2000-594306/56.  
XX  
DR N-PSDB; AAA88438.  
XX

PT Novel AXOR23 polypeptide and polynucleotides which are members of  
PT G-protein coupled (7 transmembrane) receptors for treating infections,  
PT pain, cancer, diabetes, obesity, Parkinson's disease and Huntington's  
PT disease  
XX  
XX  
PS Claim 1(a): Page 28-29; 34pp; English.  
XX  
CC The present sequence is that of a novel human G protein coupled (7  
CC transmembrane) receptor, termed AXOR23, which shows homology to  
CC GPRX, OR1A. The invention relates to AXOR23 polypeptides and  
CC polynucleotides, recombinant materials and methods for their  
CC production. Such polypeptides and polynucleotides are useful for  
CC treating bacterial, fungal, protozoan and viral infections,  
CC particularly infections caused by HIV-1 or HIV-2, pain, cancer,  
CC diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease,  
CC acute heart failure, hypotension, hypertension, urinary retention,  
CC osteoporosis, angina pectoris, myocardial infarction, stroke, ulcer,  
CC allergy, benign prostatic hypertrophy, migraine, vomiting, psychotic  
CC and neurological disorders, and dyskinesias such as Huntington's  
CC disease or Gilles de la Tourette's syndrome. They are also useful  
CC for identifying agonists and antagonists, which are useful for  
CC treating conditions associated with AXOR23 imbalance, as diagnostic  
CC reagents, for screening of genetic mutations, for chromosome  
CC localization studies, for tissue expression studies, for low  
CC capacity screening and in high-throughput screening formats, for  
CC identifying membrane bound or soluble receptors, to confound  
CC screening methods for detecting the effect of added compounds on  
CC the production of mRNA and polypeptide in cells, and as vaccines.  
XX  
XX Sequence 368 AA:  
SQ  
Query Match 18.9%; Score 438.5; DB 21; Length 368;  
Best Local Similarity 31.8%; Pred. No. 4e-36;  
Matches 127; Conservative 55; Mismatches 146; Indels 71; Gaps 14;

QY 40 ASE---SVALFEMLLDITAVAGNAAMAVIAKTPALRKFVEVHCLVDLAAITLMP 96  
DB 9 ASEVAGSLGLIAAVEVAGALLGVVLTPTGLRDALYLALHCVDLLAAASIMPL 68  
QY 97 AMLSSAL-FDHALRGEVACRLYLPLSVCSLALSVSAINVERIYVYHPRREYKMT 155  
DB 69 GLLAAPPPLGIVRRLGAPRCRAARFLSALLPACTIGVAAALGARLYLHPRGSRPP 128  
QY 156 LGLVASVLGVVWKALAMASVPLGRVMEGAPSVPCSLQMSHSAVCOI-----F 208  
DB 129 PVL---VLRAVMAAGLLDALSL-----GPPAPPPA-----PARCSVLAGGLFP 172  
QY 209 VVFAVLYLPLLLILVYCSMFVRAVAAHQGPLPTWMTTPRQSRSESLSRSTMVTS 268  
DB 173 RPLMALALFALPALLLLGAYGIFVVARRAALR-PPRPA--RCSRRLSDSLDRLSL-- 227  
QY 269 SGAPOTTPHRTGGGKAAYVLLAVGQFLCMLPRFSFHLVYALASQPISTGVESEVVM 328  
DB 228 ---PPLRPR--LPGKAALAPALAAVQFAACWLPY-----GCACIAPARAAMAAEAVVM 277  
QY 329 IGYFCTSNPFYGCILNRIQIR---GELSKQVCFEKPAPDEELRLPSRGSTIBENLQFL 385  
DB 278 VAYSNAFAPFLYGLQRYVRLALGRLSRAL---PGVVR----- 314  
QY 386 QGTGCPSESVWSRPLPSRQPEPPAVDFRIQGIATETSE 424  
DB 315 ---ACTPQAMHPRALLQCLQRPPEGPVAVGPSEAPQETPE 350

RESULT 13  
AAV71293  
ID AAV71293 standard; Protein; 368 AA.  
AC AAV71293;  
XX  
XX 02-NOV-2000 (first entry)  
XX  
XX Human orphan G protein-coupled receptor hARE-5.  
DE

XX  
XX Human: orphan G protein-coupled receptor; GPCR; hARE-5; drug screening;  
KW transmembrane receptor; signal cascade.  
XX  
XX Homo sapiens.  
XX  
XX WO200031258-A2.  
XX  
XX 02-JUN-2000.  
XX  
XX 13-OCT-1999; 99WO-US23687.  
XX  
XX 20-NOV-1998; 98US-0109213.  
XX 16-FEB-1999; 99US-0120416.  
XX 26-FEB-1999; 99US-0121852.  
XX 12-MAR-1999; 99US-0123946.  
XX 12-MAR-1999; 99US-0123949.  
XX 28-MAY-1999; 99US-0136436.  
XX 28-MAY-1999; 99US-0136437.  
XX 28-MAY-1999; 99US-0136439.  
XX 28-MAY-1999; 99US-0136567.  
XX 28-MAY-1999; 99US-0137127.  
XX 28-MAY-1999; 99US-0137131.  
XX 29-JUN-1999; 99US-0141448.  
XX 29-SEP-1999; 99US-0156555.  
XX 29-SEP-1999; 99US-0156633.  
XX 29-SEP-1999; 99US-0156634.  
XX 29-SEP-1999; 99US-0156653.  
XX 01-OCT-1999; 99US-0157280.  
XX 01-OCT-1999; 99US-0157281.  
XX 01-OCT-1999; 99US-0157282.  
XX 01-OCT-1999; 99US-0157293.  
XX 01-OCT-1999; 99US-0157294.  
XX 12-OCT-1999; 99US-0416760.  
XX 12-OCT-1999; 99US-0417044.  
XX  
XX (AREN-) ARENA PHARM INC.  
XX  
XX Chen R, Dang HT, Llaw CW, Lin I;  
XX WPI; 2000-400068/34.  
XX  
XX N-PSDB; AAD01120.  
XX  
XX Novel human orphan G protein-coupled receptors and the encoding cDNAs  
XX for use in the identification of G protein-coupled receptor agonists -  
XX  
XX Claim 10: Page 50-51; 102pp; English.  
XX  
XX The present amino acid sequence is the hARE-5, an endogenous human  
XX orphan G protein-coupled receptor (GPCR). The full length cDNA was cloned  
XX by PCR using hARE-5 specific primers and human genomic DNA as template.  
XX The orphan GPCR of the invention, like all GPCRs has seven transmembrane  
XX alpha helices with an extracellular N-terminus and an intracellular  
XX C-terminus. However, no endogenous ligands has yet been identified for  
XX the proteins of the invention. The orphan GPCRs may be used in the  
XX identification of their endogenous ligands, and to screen potential GPCR  
XX agonists and antagonists for use as pharmaceutical agents. The proteins  
XX may also be used in the study of GPCR-mediated signalling cascades, and  
XX to elucidate their precise role in normal and diseased human conditions.  
XX Nucleic acid encoding human orphan GPCRs may be used for tissue  
XX localisation expression analysis to provide information about their  
XX function in healthy and pathological states.  
XX  
XX Sequence 368 AA:  
SQ  
Query Match 18.9%; Score 438.5; DB 21; Length 368;  
Best Local Similarity 31.8%; Pred. No. 4e-36;  
Matches 127; Conservative 55; Mismatches 146; Indels 71; Gaps 14;

QY 40 ASE---SVALFEMLLDITAVAGNAAMAVIAKTPALRKFVEVHCLVDLAAITLMP 96  
DB 9 ASEVAGSLGLIAAVEVAGALLGVVLTPTGLRDALYLALHCVDLLAAASIMPL 68

```

OY 97 AMLSSAL-FDHALFGEVACRLYLFLSVCFSALISVAINVERYYVHPMREVRMT 155
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 69 GLLAAPPCGLGVRIGPACRAARPLSALLPACTLGVALLARLRLVHPLRGSRPP 128
OY 156 LGLVASVLGVVWVKALAMASVPLGRVSWEGAPSVPGCSLQMSHAYCOL-----F 208
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 129 PVL---VLTAAVMAAGLLGALSLL-----GPPAPPPA-----PARCSVLAGLGPF 172
OY 209 VVVFVAVLYFLPLLILLYVYCSMFYARVAAMOHGPLPTWMENPRORSLSRSRTMYS 268
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 173 RPLMALFLAFALPALLLGLAVGIGFVYARARALR-PPRPA--RGSRLRSDLSRLSIL-- 227
OY 269 SCAPQTPPHRTFGCGKAAYVLLAVGQFLLCMLPYFSFHLVYALSNOPISTQVESVTM 328
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 228 ---PPLRPR--LPGCKAALAPALAVGQFAACMLPY-----GCACLAAPARAABEAAYTM 277
OY 329 IGYFCFTSNPFYFGCLNQIR---GELSKQVYCFKRPAPDEELRLPSREGSIEENFLOFL 385
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 278 VAVSAFAAHPLFLYGLQRPVRLALGRLSRRL-----PGVVR----- 314
OY 386 QGTGCPSESWSRPLPSPKQEPYAVDFRIPQIAETSE 424
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 315 ---ACTPQAMHPRALLQCLQRPPEGPVANGSPSEAPQTPPE 350

```

```

RESULT 14
AAB02827
ID AAB02827 standard: protein; 368 AA.

```

```

XX AAB02827:

```

```

DT 22-AUG-2000 (first entry)

```

```

XX Human G protein coupled receptor hare-5 protein seq ID NO:6.

```

```

KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW Identification; agonist; screening; therapeutic; pharmaceutical;
KW mutant.

```

```

XX Homo sapiens.

```

```

PM WO200022131-A2.

```

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PD 20-APR-2000.

```

```

PE 13-OCT-1999; 99WO-US24065.

```

```

XX 13-OCT-1998; 98US-0170496.

```

```

PR 12-NOV-1998; 98US-0108029.

```

```

PR 20-NOV-1998; 98US-0109213.

```

```

PR 27-NOV-1998; 98US-0110060.

```

```

PR 16-FEB-1999; 99US-0120416.

```

```

PR 26-FEB-1999; 99US-0121852.

```

```

PR 12-MAR-1999; 99US-0123944.

```

```

PR 12-MAR-1999; 99US-0123945.

```

```

PR 12-MAR-1999; 99US-0123946.

```

```

PR 12-MAR-1999; 99US-0123948.

```

```

PR 12-MAR-1999; 99US-0123949.

```

```

PR 12-MAR-1999; 99US-0123951.

```

```

PR 28-MAY-1999; 99US-0136436.

```

```

PR 28-MAY-1999; 99US-0136437.

```

```

PR 28-MAY-1999; 99US-0136439.

```

```

PR 28-MAY-1999; 99US-0137127.

```

```

PR 28-MAY-1999; 99US-0137131.

```

```

PR 28-MAY-1999; 99US-0137567.

```

```

PR 30-JUN-1999; 99US-0141448.

```

```

PR 27-AUG-1999; 99US-0151114.

```

```

PR 03-SEP-1999; 99US-0152524.

```

```

PR 29-SEP-1999; 99US-0156633.

```

```

PR 29-SEP-1999; 99US-0156555.

```

```

PR 29-SEP-1999; 99US-0156634.

```

```

XX (AREN-) ARENA PHARM INC.

```

```

XX Behan DP, Lehmann-Brulsma K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX WPI: 2000-317986/27.
DR N-PSDB: AAA46019.
XX Non-endogenous, human G protein-coupled receptors for screening
PT receptor, inverse or partial agonists useful as therapeutic agents
PS Example 1; Page 79-80; 187pp; English.

```

The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically, the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the exemplification of the present invention.

```

XX Sequence 368 AA:

```

```

Query Match 18.9%; Score 438.5; DB 21; Length 368;
Best Local Similarity 31.8%; Pred. No. 4e-36;
Matches 127; Conservative 55; Mismatches 146; Indels 71; Gaps 14;

```

```

OY 40 ASE---SVALFPMLLDITAVAGNAVAVIKTRALRFVVFHCLVDLLAALTML 96
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 9 ASEVAGSLGLILAAVVEGALLNGALLVVLRTPLGRLDYLALHCVDDLAASIMPL 68

```

```

OY 97 AMLSSAL-FDHALFGEVACRLYLFLSVCFSALISVAINVERYYVHPMREVRMT 155
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 69 GLLAAPPCGLGVRIGPACRAARPLSALLPACTLGVALLARLRLVHPLRGSRPP 128

```

```

OY 156 LGLVASVLGVVWVKALAMASVPLGRVSWEGAPSVPGCSLQMSHAYCOL-----F 208
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 129 PVL---VLTAAVMAAGLLGALSLL-----GPPAPPPA-----PARCSVLAGLGPF 172

```

```

OY 209 VVVFVAVLYFLPLLILLYVYCSMFYARVAAMOHGPLPTWMENPRORSLSRSRTMYS 268
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 173 RPLMALFLAFALPALLLGLAVGIGFVYARARALR-PPRPA--RGSRLRSDLSRLSIL-- 227

```

```

OY 269 SCAPQTPPHRTFGCGKAAYVLLAVGQFLLCMLPYFSFHLVYALSNOPISTQVESVTM 328
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 228 ---PPLRPR--LPGCKAALAPALAVGQFAACMLPY-----GCACLAAPARAABEAAYTM 277

```

```

OY 329 IGYFCFTSNPFYFGCLNQIR---GELSKQVYCFKRPAPDEELRLPSREGSIEENFLOFL 385
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 278 VAVSAFAAHPLFLYGLQRPVRLALGRLSRRL-----PGVVR----- 314

```

```

OY 386 QGTGCPSESWSRPLPSPKQEPYAVDFRIPQIAETSE 424
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 315 ---ACTPQAMHPRALLQCLQRPPEGPVANGSPSEAPQTPPE 350

```

```

RESULT 15

```

```

ID AAB02827 standard: protein; 368 AA.

```

```

XX AAB02827:

```

```

DT 25-JAN-2002 (first entry)

```

```

XX G-protein coupled receptor (GPCR) #4.

```

```

PR G-protein coupled receptor; GPCR; vaccine; gene therapy;
PR cell proliferation disorder; cancer; arteriosclerosis;
PR neurological disorder; epilepsy; stroke; cardiovascular disorder;
PR hypertension; ischemic heart disease; gastrointestinal disorder;
PR anorexia; peptic ulcer; autoimmune disorder; inflammatory disorder;
PR diabetes; osteoporosis; psoriasis; metabolic disorder; obesity;

```

```

KW (AREN-) ARENA PHARM INC.

```



KM schizophrenic disorder; neuroskeletal disorder.  
XX  
OS Homo sapiens.  
XX  
PM WO20016742-A2.  
XX  
PD 13-SEP-2001.  
XX  
PF 01-MAR-2001; 2001WO-US06814.  
XX  
PR 03-MAR-2000; 2000US-186854P.  
XX  
PR 10-MAR-2000; 2000US-188384P.  
PR 17-MAR-2000; 2000US-190453P.  
PR 20-MAR-2000; 2000US-190730P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Lal P, Tang YT, Patterson C, Yao MG, Shih LL, Tribouley CM;  
PI Lu DM, Yue H, Khan FA, Policky JL, Au-Young J, Yang J;  
PI Harland L, Walsh RT, Lo TP, Borowsky ML;  
XX  
XX WPI: 2001-656776/75.  
DR N-PSDB; AAS15900.  
XX  
PT Novel G-protein coupled receptor polypeptides, for treating and  
PT preventing autoimmune/inflammatory disorders, neurological disorders,  
PT cell proliferative disorders, cardiovascular disorders and viral  
PT infections .  
XX  
PS Claim 1; Page 116-117; 141pp; English.  
XX  
XX The invention describes a novel isolated polypeptide, selected from a  
CC group of 21 G-protein coupled receptor polypeptides (GCREC) and useful in  
CC vaccines and gene therapy. The polypeptide (I) is useful for screening  
CC for agonist or antagonist of (I), compounds specifically binding to (I),  
CC or compounds that modulate the activity of (I). The polynucleotide  
CC encoding (I) is useful for screening a compound for effectiveness in  
CC altering expression of a target polynucleotide comprising (II), by  
CC exposing a sample comprising the target polynucleotide to a compound,  
CC detecting altered expression of the target polynucleotide, and comparing  
CC the expression of the target polynucleotide in the presence of varying  
CC amounts of compound and in the absence of the compound. (I) and (II) are  
CC useful for diagnosis, treatment and prevention of cell proliferative  
CC disorders (e.g. cancers, arteriosclerosis, atherosclerosis, neurological  
CC disorders (e.g. epilepsy, stroke, schizophrenic disorders and  
CC neuroskeletal disorders), cardiovascular disorders (e.g. hypertension,  
CC ischaemic heart disease), gastrointestinal disorders (e.g. anorexia,  
CC peptic ulcer), autoimmune/inflammatory disorders (e.g. diabetes mellitus,  
CC osteoporosis, psoriasis), and metabolic disorders such as obesity.  
CC Furthermore, the polynucleotide is useful as primers for detecting  
CC single nucleotide polymorphisms; as elements in microarray, to monitor or  
CC measure protein-protein interactions, drug-target interactions, and gene  
CC expression profiles; to generate a transcript image of a tissue or cell  
CC type, and to generate hybridisation probes useful in mapping the  
CC naturally occurring genomic sequence. This is the G-protein coupled  
CC receptor 4 (GCREC-4), one of 21 GCREC proteins described in the method of  
CC the invention.  
XX  
SQ Sequence 368 AA:  
Query Match 18.9%; Score 438.5; DB 22; Length 368;  
Best Local Similarity 31.8%; Pred. No. 4e-36;  
Matches 127; Conservative 55; Mismatches 146; Indels 71; Gaps 14;  
QY 40 ASE---SVALFPMILDTAVAGNAAMVIAKTPALRKEVFVHLCIVDLLAATLMP 96  
DB 9 ASEVAGSLGLIAAVVEGALNGALLVVRTPGLRDALYIAHLCVVDLLAASIMPL 68  
QY 97 AMLSSAL-FDHALGGEVACRLXFLSYVCSVALISVAINVERIYVYVHPRKEVRMT 155  
DB 69 GLLAAPPPEGLGVNRGPAPCARARFLSALLPACTGLGVALGLIARLIVHPLRGSRPP 128  
QY 156 LGIVASVLEGVVVKALAMASVPLGRVSWEGAPSVPCSLQWSHAYCQL-----F 208

DB 129 PVL---VLTAAVMAAGLGLSL-----GPPAPPPA-----PARCSVLAGLGP 172  
QY 209 VVFAVLFLDLPLLILVYCGMFRVAVAMQHGLPTWMETPRORSLSRSTMTWS 268  
DB 173 RPLMALAFALPALLLGAYGGIFVVARRAALR-PPRA--RGSRLRSDLSRLSL-- 227  
QY 269 SGAPQTPHRTGGGKAADVLLAVGGQFLCWLPEFSFLVYALSAQPISTGQVESVYTW 328  
DB 228 ---PPLRPR--LPGKAALAPALAVGQFAACWLPY-----GCACLPARAADAEAVTW 277  
QY 329 IGYFCTSNPFYGCINRQIR---GELSKQFVCFKPAPEEBRLRPSRGSIENFLOPL 385  
DB 278 VAYSAPFAHPLFLYGLQRPVRLALGRLSRAL-----PGVYR----- 314  
QY 386 QGTGCPSESWSVRPLPSPKQPPAVDFRIPGQIAETSE 424  
DB 315 ---ACTPQAMHPRALLQCLQRPPEGPAPVSPSEAPETPTE 350

Search completed: October 21, 2002, 16:09:24  
Job time : 38 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2002, 16:08:10 ; Search time 17 Seconds  
(without alignments)  
647.997 Million cell updates/sec

Title: US-09-838-028-2

Perfect score: 2318  
Sequence: 1 MESSPIPOSGNSSTLGRVP.....SDIIMSDYLPRASPRLS 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/plodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/plodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/plodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/plodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/plodata/1/1aa/PCUOS\_COMB.pep:\*  
6: /cgn2\_6/plodata/1/1aa/Backfilest.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
No.							
1	1276	55.0	252	3	US-08-513-974B-52		Sequence 52, Appl
2	1276	55.0	252	3	US-08-513-974B-360		Sequence 360, App
3	351	15.1	358	2	US-08-748-485-6		Sequence 6, Appli
4	350	15.1	359	2	US-08-103-170-7		Sequence 7, Appli
5	349	15.1	359	1	US-07-996-772A-10		Sequence 10, Appli
6	349	15.1	359	2	US-08-748-485-3		Sequence 3, Appli
7	347	15.0	348	4	US-08-875-540-13		Sequence 13, Appli
8	347	15.0	348	4	US-09-171-456-17		Sequence 17, Appli
9	346	14.9	359	2	US-08-103-170-6		Sequence 4, Appli
10	346	14.9	359	2	US-08-103-170-6		Sequence 6, Appli
11	343	14.8	359	2	US-08-748-485-5		Sequence 5, Appli
12	340	14.7	359	2	US-08-467-568-13		Sequence 13, Appli
13	340	14.7	359	2	US-08-748-485-4		Sequence 4, Appli
14	340	14.7	359	2	US-08-103-170-2		Sequence 2, Appli
15	340	14.7	359	2	US-09-030-582-13		Sequence 13, Appli
16	340	14.7	359	3	US-08-875-540-15		Sequence 15, Appli
17	340	14.7	359	4	US-09-171-456-19		Sequence 19, Appli
18	337	14.5	400	1	US-07-916-901-6		Sequence 6, Appli
19	336	14.5	400	1	US-07-783-602C-1		Sequence 1, Appli
20	335.5	14.5	405	1	US-08-351-473B-2		Sequence 2, Appli
21	335	14.5	400	1	US-08-351-473B-4		Sequence 4, Appli
22	332.5	14.3	572	1	US-08-334-698-2		Sequence 2, Appli
23	332.5	14.3	572	1	US-08-228-932-2		Sequence 2, Appli
24	332.5	14.3	572	1	US-08-468-939-2		Sequence 2, Appli
25	332.5	14.3	572	1	US-08-722-001-30		Sequence 30, Appli
26	332.5	14.3	572	1	US-08-406-855A-2		Sequence 2, Appli
27	332.5	14.3	572	2	US-08-722-190-2		Sequence 2, Appli

28	332.5	14.3	572	3	US-08-244-354-2	Sequence 2, Appli
29	332.5	14.3	572	3	US-09-206-899-2	Sequence 2, Appli
30	332.5	14.3	572	5	PCT-US95-0403-2	Sequence 2, Appli
31	326.5	14.1	388	1	US-08-087-772A-2	Sequence 2, Appli
32	326.5	14.1	400	1	US-08-351-473B-5	Sequence 5, Appli
33	326.5	14.1	400	4	US-08-450-962-4	Sequence 4, Appli
34	326.5	14.1	400	4	US-08-450-962-6	Sequence 6, Appli
35	321	13.8	559	2	US-08-406-855A-20	Sequence 20, Appli
36	321	13.8	559	3	US-07-206-889-20	Sequence 20, Appli
37	320	13.8	501	1	US-08-722-001-14	Sequence 14, Appli
38	320	13.8	501	2	US-08-467-568-9	Sequence 9, Appli
39	320	13.8	501	2	US-09-030-582-9	Sequence 9, Appli
40	319.5	13.8	402	1	US-08-444-734A-6	Sequence 6, Appli
41	319.5	13.8	402	1	US-08-087-772A-15	Sequence 15, Appli
42	319.5	13.8	408	1	US-07-916-901-2	Sequence 2, Appli
43	319.5	13.8	408	1	US-08-351-473B-3	Sequence 3, Appli
44	319.5	13.8	408	4	US-08-450-962-2	Sequence 2, Appli
45	319.5	13.8	408	4	US-08-450-962-5	Sequence 5, Appli

#### ALIGNMENTS

RESULT 1  
US-08-513-974B-52  
Sequence 52, Application US/08513974B  
Patent No. 6114139  
GENERAL INFORMATION:  
APPLICANT: Hinuma, Shuji  
APPLICANT: Hosoya, Masaki  
APPLICANT: Fujii, Ryo  
APPLICANT: Ohtaki, Tetsuya  
APPLICANT: Fukusumi, Shoji  
APPLICANT: Ohgi, Kazuhiko  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
NUMBER OF SEQUENCES: 380  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513, 974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357

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: FILING DATE: 30-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-236356
: FILING DATE: 30-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-189274
: FILING DATE: 11-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-189273
: FILING DATE: 11-AUG-1945
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-189272
: FILING DATE: 11-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Resnick, David S.
: REGISTRATION NUMBER: 34,235
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-523-3400
: TELEFAX: 617-523-6440
: INFORMATION FOR SEQ ID NO: 52:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 252 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-513-974B-52
```

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Query Match          55.0%; Score 1276; DB 3; Length 252;
Best Local Similarity 98.0%; Pred. No. 1,3e-92;
Matches 247; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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QY 85 VDLAALTPLMLAMSSALFDHALFGEVACRLYLFLSCFVSLAITSVSAINVERYYV 144
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DB 1 VDLAALTPLMLAMSSALFDHALFGEVACRLYLFLSCFVSLAITSVSAINVERYYV 60
   |||||||
QY 145 VHPMRYEVRMTLGLVASYLVGVWVKALAMASVPLGVRVSWEGAPSPVPGCSLQWHSAY 204
   |||||||
DB 61 VHPMRYEVRMTLGLVASYLVGVWVKALAMASVPLGVRVSWEGAPSPVPGCSLQWHSAY 120
   |||||||
QY 205 COLVVVFAVLYFLPLLLILVYCSMRVARVAMOHGRLPTMWTETROSESLSNST 264
   |||||||
DB 121 COLVVVFAVLYFLPLLLILVYCSMRVARVAMOHGRLPTMWTETROSESLSNST 180
   |||||||
QY 265 WYSSGAGQTPPHRTFEGGKAAVYLLAVGGQFLCMLPFSPFLYVALSAQPISTGVES 324
   |||||||
DB 181 WYSSGAGQTPPHRTFEGGKAAVYLLAVGGQFLCMLPFSPFLYVALSAQPIAGOVEN 240
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QY 325 VVTWIGYFCFTS 336
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DB 241 VVTWIGYFCFTS 252
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RESULT 2
US-08-513-974B-360
: Sequence 360, Application US/08513974B
: Patent No. 6114139
: GENERAL INFORMATION:
: APPLICANT: Hinuma, Shuji
: APPLICANT: Hosoya, Masaki
: APPLICANT: Fujii, Ryo
: APPLICANT: Ohtaki, Tetsuya
: APPLICANT: Fukusumi, Shoji
: APPLICANT: Ohgi, Kazuhiko
: TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
: NUMBER OF SEQUENCES: 380
: TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
: STREET: 130 Water Street
: CITY: Boston
: STATE: MA
```

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: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/513,974B
: FILING DATE: 14-SEP-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/JP95/01599
: FILING DATE: 10-AUG-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 7-093989
: FILING DATE: 19-AUG-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 7-057186
: FILING DATE: 16-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 7-007177
: FILING DATE: 20-JAN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-326611
: FILING DATE: 28-DEC-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-270017
: FILING DATE: 02-NOV-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-236357
: FILING DATE: 30-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-236356
: FILING DATE: 30-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-189274
: FILING DATE: 11-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-189273
: FILING DATE: 11-AUG-1945
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-189272
: FILING DATE: 11-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Resnick, David S.
: REGISTRATION NUMBER: 34,235
: REFERENCE/DOCKET NUMBER: 45753
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-523-3400
: TELEFAX: 617-523-6440
: INFORMATION FOR SEQ ID NO: 360:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 252 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-513-974B-360
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Query Match          55.0%; Score 1276; DB 3; Length 252;
Best Local Similarity 98.0%; Pred. No. 1,3e-92;
Matches 247; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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QY 85 VDLAALTPLMLAMSSALFDHALFGEVACRLYLFLSCFVSLAITSVSAINVERYYV 144
   |||||||
DB 1 VDLAALTPLMLAMSSALFDHALFGEVACRLYLFLSCFVSLAITSVSAINVERYYV 60
   |||||||
QY 145 VHPMRYEVRMTLGLVASYLVGVWVKALAMASVPLGVRVSWEGAPSPVPGCSLQWHSAY 204
   |||||||
DB 61 VHPMRYEVRMTLGLVASYLVGVWVKALAMASVPLGVRVSWEGAPSPVPGCSLQWHSAY 120
   |||||||
QY 205 COLVVVFAVLYFLPLLLILVYCSMRVARVAMOHGRLPTMWTETROSESLSNST 264
   |||||||
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Db 121 COLFVVEAVLLELLPLLLIIVVCSMFVRVAVAAHGPPTMETPRORSESLSSRST 180  
 Oy 265 WVTSSGAPQTPHRTFGGKAIVLLAVGGOLCWLPRFPHLVALSAGQISTGQVES 324  
 Db 181 WVTSSGAPQTPHRTFGGKAIVLLAVGGOLCWLPRFPHLVALSAGQISTGQVES 240  
 Oy 325 VVTWIGYFCFTS 336  
 Db 241 VVTWIGYFCFTS 252

RESULT 3  
 US-08-748-485-6  
 : Sequence 6, Application US/08748485  
 : Patent No. 5817480  
 :  
 : GENERAL INFORMATION:  
 : APPLICANT: Au-Young, Janice.  
 : APPLICANT: Guegler, Karl J.  
 : APPLICANT: Goli, Surya K.  
 : APPLICANT: Murty, Lynn E.  
 : TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR  
 : NUMBER OF SEQUENCES: 8  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 : STREET: 3174 Porter Drive  
 : CITY: Palo Alto  
 : STATE: CA  
 : COUNTRY: US  
 : ZIP: 94304  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : COMPUTER: IBM Compatible  
 : OPERATING SYSTEM: DOS  
 : SOFTWARE: FASTSEQ Version 2.0  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/748,485  
 : FILING DATE: Herewith  
 : CLASSIFICATION: 530  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER:  
 : FILING DATE:  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Billings, Lucy J.  
 : REGISTRATION NUMBER: 36,749  
 : REFERENCE/DOCKET NUMBER: PR-0159 US  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 415-855-0555  
 : TELEFAX: 415-845-4166  
 : TELEX:  
 : INFORMATION FOR SEQ ID NO: 6:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 358 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : IMMEDIATE SOURCE:  
 : LIBRARY: Genbank  
 : CLONE: 236184  
 : US-08-748-485-6

Query Match 15.1%; Score 351; DB 2; Length 358;  
 Best Local Similarity 27.5%; Pred. No. 4.1e-20;  
 Matches 106; Conservative 58; Mismatches 150; Indels 72; Gaps 12;

Db 43 SVAFEMLLDLTAVAGAAVAVIAKTPALRKYV--FVPHLCVLDLLAATLPLMLAMS 100  
 Oy 22 SVVLTTLILI--TLAGNVVVCIAVSLNRRLSLTNCFTIVSLAANDLLGLLVPF---- 74  
 Oy 101 SSALEFDHAL---FGEVACRLTFLFSCVSLAIVSAINVERRYVVVHPARIEVRLGL 157  
 Db 75 -SAIQSLFTWSFGHVFENITSLDVLMLCTASILNLFMISIDRCYCAVDPRLVPLVPV 133  
 Oy 158 LVASVLGVWVKALAMASVPLVGRVSWEE-----GAPSVPGGSLQMSHSAYCOLFVVV 211

Db 134 RVALSLVEFIWVISTLSLST--HIGMNSRNGCTRGNGNFFK--CAVQVN-----EVLGLV 184  
 Oy 212 FAVLYELLPLLLIIVVCSMFVRVAVAAHGPPTMETPRORSESLSSRSTWVTSSGA 271  
 Db 185 DGLVTFYLLPLLMCVTYRIFRIAREQAKRINHISMMKAA----- 224  
 Oy 272 PQTTPHRTFGGKAIVLLAVGGOLCWLPRFPHLVALSAGQISTGQVESVYTWIGY 331  
 Db 225 -----TIREHKATVTTLAAVWGAFTICWPFYFAFVYRGLGDDAINEAVEGVLWLG 277  
 Oy 332 FCFTSNPFYGCINRIGELSKOPVCFKP--APEELRL-----PSREGSIEENF 381  
 Db 278 ANSALNPLIYLAALNDFRTAQQLEPHCKFASHNSHKTSRLNLSLPSQSREGWQLEK 337  
 Oy 382 LQFLQGTGCPSPESVSRPLPSPKQEP 407  
 Db 338 PLKIQ-----VMSGTELTHPQGNP 356

RESULT 4  
 US-08-103-170-7  
 : Sequence 7, Application US/08103170  
 : Patent No. 5885824  
 :  
 : GENERAL INFORMATION:  
 : APPLICANT: Yamada, Tadataka  
 : APPLICANT: Gantz, Ira  
 : TITLE OF INVENTION: Recombinant Genomic Clones Encoding  
 : TITLE OF INVENTION: Histamine H1, H2, and H3 Receptors, Methods for Production  
 : TITLE OF INVENTION: Thereof, and Proteins Encoded Therefrom  
 : NUMBER OF SEQUENCES: 41  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 : ADDRESS: P.C.  
 : STREET: 1755 Jefferson Davis Highway, Fourth Floor  
 : CITY: Arlington  
 : STATE: Virginia  
 : COUNTRY: U.S.A.  
 : ZIP: 22202  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/103,170  
 : FILING DATE:  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/633,060  
 : FILING DATE: 24-DEC-1990  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Lavalleye, Jean-Paul  
 : REGISTRATION NUMBER: 31,451  
 : REFERENCE/DOCKET NUMBER: 2363-017-55  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (703)521-4500  
 : TELEFAX: (703)486-2347  
 : TELEX: 24885 OPAT UR  
 : INFORMATION FOR SEQ ID NO: 7:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 359 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: unknown  
 : MOLECULE TYPE: protein  
 : ORIGINAL SOURCE:  
 : ORGANISM: Dog  
 : US-08-103-170-7

Query Match 15.1%; Score 350; DB 2; Length 359;  
 Best Local Similarity 28.7%; Pred. No. 4.9e-20;  
 Matches 100; Conservative 56; Mismatches 140; Indels 52; Gaps 10;

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: RESULT 5
: US-07-996-772A-10
: Sequence 10: Application US/07996772A
: Patent No. 5472866
: GENERAL INFORMATION:
: APPLICANT: Gerald, Christophe
: APPLICANT: Hartig, Paul R.
: APPLICANT: Branchek, Theresa A.
: APPLICANT: Welshank, Richard L.
: TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN
: TITLE OF INVENTION: RECEPTORS AND USES THEREOF
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: COOPER & DUNHAM
: STREET: 30 ROCKEFELLER PLAZA
: CITY: NEW YORK
: STATE: NEW YORK
: ZIP: 10112
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/996,772A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: White, P., John
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 42667/JWP/TEP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 977-9550
: TELEFAX: (212) 664-0525
: TELEX: 422523 COOP UI
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 359 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: IMMEDIATE SOURCE:
: CLONE: HIST2
: ?
: ?
: US-07-996-772A-10

```

```

1      RESULT 6
2      US-08-748-485-3
3      : Sequence 3, Application US/08748485
4      : Patent No. 5817480
5      : GENERAL INFORMATION:
6      : APPLICANT: Au-Young, Janice
7      : APPLICANT: Guegler, Karl J.
8      : APPLICANT: Goll, Surya K.
9      : APPLICANT: Murty, Lynn E.
10     : TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR
11     : NUMBER OF SEQUENCES: 8
12     : CORRESPONDENCE ADDRESS:
13     : ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
14     : STREET: 3174 Porter Drive
15     : CITY: Palo Alto
16     : STATE: CA
17     : COUNTRY: US
18     : ZIP: 94304
19     : COMPUTER READABLE FORM:
20     : MEDIUM TYPE: Diskette
21     : COMPUTER: IBM Compatible
22     : OPERATING SYSTEM: DOS
23     : SOFTWARE: FastSeq Version 2.0
24     : CURRENT APPLICATION DATA:
25     : APPLICATION NUMBER: US/08/748,485
26     : FILING DATE: Herewith
27     : CLASSIFICATION: 530
28     : PRIOR APPLICATION DATA:
29     : APPLICATION NUMBER:
30     : FILING DATE:
31     : ATTORNEY/AGENT INFORMATION:
32     : NAME: Billings, Lucy J.
33     : REGISTRATION NUMBER: 36,749
34     : REFERENCE/DOCKET NUMBER: PE-0159 US
35     : TELECOMMUNICATION INFORMATION:
36     : TELEPHONE: 415-855-0555
37     : TELEFAX: 415-845-4166
38     :
39     : TELEX:
40     : INFORMATION FOR SEQ ID NO: 3:
41     : SEQUENCE CHARACTERISTICS:
42     : LENGTH: 359 amino acids
43     : TYPE: amino acid
44     : STRANDEDNESS: single
45     : TOPOLOGY: linear
46     : IMMEDIATE SOURCE:
47     : LIBRARY: Genbank
48     :
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100    :

```



;; TITLE OF INVENTION: Recombinant Genomic Clones Encoding  
;; TITLE OF INVENTION: Histamine H1, H2, and H3 Receptors, Methods For Production  
;; TITLE OF INVENTION: Thereof, and Proteins Encoded Therefrom  
;; NUMBER OF SEQUENCES: 41  
;; CORRESPONDENCE ADDRESSES:  
;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,  
;; ADDRESS: P.C.  
;; STREET: 1755 Jefferson Davis Highway, Fourth Floor  
;; CITY: Arlington  
;; STATE: Virginia  
;; COUNTRY: U.S.A.  
;; ZIP: 22202  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/103,170  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/633,060  
;; FILING DATE: 24-DEC-1990  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Lavalleye, Jean-Paul  
;; REGISTRATION NUMBER: 31,451  
;; REFERENCE/DOCKET NUMBER: 2363-017-55  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (703)521-4500  
;; TELEFAX: (703)486-2347  
;;  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 359 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;;  
;; US-08-103-170-4

Query Match 14.9%; Score 346; DB 2; Length 359;  
Best Local Similarity 28.7%; Pred. No. 1e-19;  
Matches 100; Conservative 55; Mismatches 141; Indels 52; Gaps 10;

QY 43 SVALFFMLLDITAVAGNAVAIAKTPALRKPV--FVFNHCLVDLLAALTIMPLAMLS 100  
DB 22 SVLVTLVLI--TLAGNVVCLAVGLNRRLRSLTNCFTIVSLAITDILLGLVLDPF---- 74  
QY 101 SSALFDHAL---FGEVACRLYLFLSVCFVSLAITSVAINVERYYVYVHPMYEVRMTLG 157  
DB 75 -SAFQOLSCRMSEFGVFCNITYTSLDVMCTASILNLFMISLDRCYAVNDPLRYPLVLTIPV 133  
QY 158 LVASLVGVWVKALAMASVPV-LGRVSWMEGAP--SVPGCSLQMSHSAVCQLFVVAV 214  
DB 134 RVAVSLVLIVWISTILSFSLHGMNSRNETSFPNHTTPKCKVQVN-----LVYGLVDGL 188  
QY 215 LVFLPLLLIILVYCSMFRVARVAMOGPLPTMMETPRORSESLSSSTWTSSGAPQT 274  
DB 169 VFVYPLPLVLCITTYRIKRIARIRHDOAKHMGSKAA----- 225  
QY 275 TPHRFEGGKAANVLAVGGOFLLCWLPPYFPHLYVALSAQPISTGOVESVYTWIGYCF 334  
DB 226 ---TIGEHKATVTLAAVWGAFTICMPFTFYVYRGKLGDDAINEAEVAVYLMIGYANS 281  
QY 335 TSNPFYGCNLNRIQIGELSKOVCFKPAPE--EELRLPSREGSTEEN 380  
DB 282 ALNPILVATLNRDFTAYQQLFRC--RPASHNAQETSLRNSSQLARN 327

;; GENERAL INFORMATION:  
;; APPLICANT: Yamada, Tadataka  
;; APPLICANT: Gantz, Ira  
;; TITLE OF INVENTION: Recombinant Genomic Clones Encoding  
;; TITLE OF INVENTION: Histamine H1, H2, and H3 Receptors, Methods For Production  
;; TITLE OF INVENTION: Thereof, and Proteins Encoded Therefrom  
;; NUMBER OF SEQUENCES: 41  
;; CORRESPONDENCE ADDRESSES:  
;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,  
;; ADDRESS: P.C.  
;; STREET: 1755 Jefferson Davis Highway, Fourth Floor  
;; CITY: Arlington  
;; STATE: Virginia  
;; COUNTRY: U.S.A.  
;; ZIP: 22202  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/103,170  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/633,060  
;; FILING DATE: 24-DEC-1990  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Lavalleye, Jean-Paul  
;; REGISTRATION NUMBER: 31,451  
;; REFERENCE/DOCKET NUMBER: 2363-017-55  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (703)521-4500  
;; TELEFAX: (703)486-2347  
;;  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 359 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;;  
;; US-08-103-170-6

Query Match 14.9%; Score 346; DB 2; Length 359;  
Best Local Similarity 28.7%; Pred. No. 1e-19;  
Matches 100; Conservative 55; Mismatches 141; Indels 52; Gaps 10;

QY 43 SVALFFMLLDITAVAGNAVAIAKTPALRKPV--FVFNHCLVDLLAALTIMPLAMLS 100  
DB 22 SVLVTLVLI--TLAGNVVCLAVGLNRRLRSLTNCFTIVSLAITDILLGLVLDPF---- 74  
QY 101 SSALFDHAL---FGEVACRLYLFLSVCFVSLAITSVAINVERYYVYVHPMYEVRMTLG 157  
DB 75 -SAFQOLSCRMSEFGVFCNITYTSLDVMCTASILNLFMISLDRCYAVNDPLRYPLVLTIPV 133  
QY 158 LVASLVGVWVKALAMASVPV-LGRVSWMEGAP--SVPGCSLQMSHSAVCQLFVVAV 214  
DB 134 RVAVSLVLIVWISTILSFSLHGMNSRNETSFPNHTTPKCKVQVN-----LVYGLVDGL 188  
QY 215 LVFLPLLLIILVYCSMFRVARVAMOGPLPTMMETPRORSESLSSSTWTSSGAPQT 274  
DB 169 VFVYPLPLVLCITTYRIKRIARIRHDOAKHMGSKAA----- 225  
QY 275 TPHRFEGGKAANVLAVGGOFLLCWLPPYFPHLYVALSAQPISTGOVESVYTWIGYCF 334  
DB 226 ---TIGEHKATVTLAAVWGAFTICMPFTFYVYRGKLGDDAINEAEVAVYLMIGYANS 281  
QY 335 TSNPFYGCNLNRIQIGELSKOVCFKPAPE--EELRLPSREGSTEEN 380  
DB 282 ALNPILVATLNRDFTAYQQLFRC--RPASHNAQETSLRNSSQLARN 327



```

US-08-748-485-5
; Sequence 5, Application US/08748485
; Patent No. 5817480
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Goli, Surya K.
; APPLICANT: Murty, Lynn E.
; TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,485
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0159 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 791239
; US-08-748-485-5

Query Match          14.8%; Score 343; DB 2; Length 359;
Best Local Similarity 27.0%; Pred. No. 1.7e-19;
Matches 99; Conservative 57; Mismatches 146; Indels 64; Gaps 11;

OY 49 MLLDLTAVAGNAAMAVIAKTPALRKFEV--FVFHLCLVDLLAALTPLMLSSALFD 106
DB 25 LILILITVAGNVVVCCLAVGLNRRLRLNCFIVSLAVTDLLGLLVLP-----SAIQY 79
OY 107 HAL---FGEVACRLYLELSCVFSALISVSAINVERIYVYVHPMRREYRMTLGLVASL 163
DB 80 LSCKSFSGKVCNITYTSLDVMICTASILNLFMISIDRYCAVMDPLRYVLTVPVVAISL 139
OY 164 VGWVKALAMASVPYLGRVSMEEGAPSVPG-----CSLQMSHSAVCOLEFVVFAVLYFL 218
DB 140 VLIWVISTLSFLST--HGMNSRNETSKNDNTIYKCKVQVN-----EYGLVDGLVTFLY 192
OY 219 LPLLILIVVYCSMFVRVAAVMOHGPLPTWMTETPRQRESESLSSRSTWVTSSGAPQTPPHR 278
DB 193 LPLLIMCTYFRIFRIAREQARRINHTGSMKAA----- 225
OY 279 TFGGKAIVVLLAAGGOFLLCWLPRYFSFHLIYVALSAQPISTGOVESVYTWIGYFCFTSNP 338
DB 226 TIREKATVTTLAAMGAFITICMPFYTFVYRGGLGDADAVNEVFDDVLMGLYANSALNP 285
OY 339 FFYGCGLNQIRGELSKQVFCFKPAPEBELRLP---SREGSIEENLQFLQGTGCPSSSW 395

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DB 286 ILYAALNRDFFRTAYHQLFCC-----RLASHNSHETSLRLNNSQ-LNNSQCEPRW 334
OY 396 -VSRPL 400
DB 335 QEDKPL 340

RESULT 12
US-08-467-568-13
; Sequence 13, Application US/08467568
; Patent No. 5817477
; GENERAL INFORMATION:
; APPLICANT: SOPPET, DANIEL R
; TITLE OF INVENTION: ADRENERGIC RECEPTOR
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,568
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-324
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-568-13

Query Match          14.7%; Score 340; DB 2; Length 359;
Best Local Similarity 28.0%; Pred. No. 3e-19;
Matches 97; Conservative 57; Mismatches 134; Indels 58; Gaps 9;

OY 49 MLLDLTAVAGNAAMAVIAKTPALRKFEV--FVFHLCLVDLLAALTPLMLSSALFD 106
DB 25 LAVLITVAGNVVVCCLAVGLNRRLRLNCFIVSLATDGLLVLP-----SAIQY 79
OY 107 HAL---FGEVACRLYLELSCVFSALISVSAINVERIYVYVHPMRREYRMTLGLVASL 163
DB 80 LSCKSFSGKVCNITYTSLDVMICTASILNLFMISIDRYCAVMDPLRYVLTVPVVAISL 139
OY 164 VGWVKALAMASVPY-LGRVSMEEGAPSV--VPGCSLQMSHSAVCOLEFVVFAVLYFLP 220
DB 140 VLIWVISTLSFLSHLGMNSRNETSKGNHTTSKCKVQVN-----EYGLVDGLVTFLY 194
OY 221 LLLILIVVYCSMFVRVAAVMOHGPLPTWMTETPRQRESESLSSRSTWVTSSGAPQTPPHR 280
DB 195 LLMCTIYFRIFKVARDDAKRIINHSSKAA-----TI 227
OY 281 GGGKAIVVLLAAGGOFLLCWLPRYFSFHLIYVALSAQPISTGOVESVYTWIGYFCFTSNPF 340
DB 228 REHKATVTTLAAMGAFITICMPFYTFVYRGGLGDADAVNEVLEAIVLMGLYANSALNP 287

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QY 341 YGCLNRQIRGELSKQVCFKPAPEEELRLPSREG---SIEENFLQ 383  
Db 288 YAAINRDFRTGYQQLFCC-----RLANRSHKTSLRNSASQ 323

## RESULT 13

US-08-748-485-4  
Sequence 4, Application US/08748485  
Patent No. 5817480  
GENERAL INFORMATION:  
APPLICANT: Au-Young, Janice  
APPLICANT: Guegler, Karl J.  
APPLICANT: Goll, Surya K.  
APPLICANT: Murty, Lynn E.  
TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: US  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/748,485  
FILING DATE: Herewith  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0159 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 359 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 184088  
US-08-748-485-4

Query Match 14.7%, Score 340; DB 2; Length 359;  
Best Local Similarity 28.0%; Pred. No. 3e-19;  
Matches 97; Conservative 57; Mismatches 134; Indels 58; Gaps 9;

QY 49 MLLDLTVAGNAAMAVIAKTPALRKVF--FVPHLCVLDLALTLPLMLSSALFD 106  
Db 25 LAVLLITVAGNVVCLAVGLNRRLRLNLTNCFIVSLATDILLGLVLPF-----SALTYQ 79  
QY 107 HAL--FGEVACRLYLFVSCFVSLATLSVSAINERYVYVHPMRVEVRMTGLVASVL 163  
Db 80 LSKKSPFGKVCNITSLDVMICTASILNLFMISIDRYCAVMDPLRYVLTVPRAVATSL 139  
QY 164 VGWVKALAMASVPV-LGRVSEBAPS--VPPGCSLQMSHSAVCQLFVVVFAVLVFLP 220  
Db 140 VLIWISTITLSFLSHLGMNSRNETSKGNHTTSCKKVQVN-----EYGLVDGLVTFLP 194  
QY 221 LLLITVYVCSNFRVARVAAHQGPLPTWNETPROMSESLSSSTWTVSSGAQPTTPHRTF 280  
Db 195 LLIMCTIYRIKFAVADQAKRINHISWMAA-----T 227

QY 281 GGGKAAYVLLAVGGOFLLCMLPYEFSFHLVVALSAQPISTGCVESVWIGYCFCTSNPF 340  
Db 228 REHKATVTLAAVMGAFITCMFPTFAFYRLGRDDDAINEVLVAIVMLGTANALNPIL 287

QY 341 YGCLNRQIRGELSKQVCFKPAPEEELRLPSREG---SIEENFLQ 383  
Db 288 YAAINRDFRTGYQQLFCC-----RLANRSHKTSLRNSASQ 323

## RESULT 14

US-08-103-170-2  
Sequence 2, Application US/08103170  
Patent No. 5885824  
GENERAL INFORMATION:  
APPLICANT: Yamada, Tadataka  
APPLICANT: Gantz, Ira  
TITLE OF INVENTION: Recombinant Genomic Clones Encoding  
TITLE OF INVENTION: Histamine H1, H2, and H3 Receptors, Methods For Production  
TITLE OF INVENTION: Thereof, and Proteins Encoded Therefrom  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 Jefferson Davis Highway, Fourth floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/103,170  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/633,060  
FILING DATE: 24-DEC-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Lavalleye, Jean-Paul  
REGISTRATION NUMBER: 31,451  
REFERENCE/DOCKET NUMBER: 2363-017-55  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)521-4500  
TELEFAX: (703)486-2347  
TELEX: 24885 OPAT UR  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 359 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-103-170-2

Query Match 14.7%, Score 340; DB 2; Length 359;  
Best Local Similarity 28.0%; Pred. No. 3e-19;  
Matches 97; Conservative 57; Mismatches 134; Indels 58; Gaps 9;

QY 49 MLLDLTVAGNAAMAVIAKTPALRKVF--FVPHLCVLDLALTLPLMLSSALFD 106  
Db 25 LAVLLITVAGNVVCLAVGLNRRLRLNLTNCFIVSLATDILLGLVLPF-----SALTYQ 79  
QY 107 HAL--FGEVACRLYLFVSCFVSLATLSVSAINERYVYVHPMRVEVRMTGLVASVL 163  
Db 80 LSKKSPFGKVCNITSLDVMICTASILNLFMISIDRYCAVMDPLRYVLTVPRAVATSL 139  
QY 164 VGWVKALAMASVPV-LGRVSEBAPS--VPPGCSLQMSHSAVCQLFVVVFAVLVFLP 220  
Db 140 VLIWISTITLSFLSHLGMNSRNETSKGNHTTSCKKVQVN-----EYGLVDGLVTFLP 194

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0Y 221 LLLLLVYVCSMERARVAAMAOMHGLPLPMMEPPRQRSSLSLSRMTSSAPQTTPTRT 260
    |||:::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 195 LLIMCTIYTRFLFKARQDAKRNHINISSMKA-----TI 227

0Y 281 GGGKAAVLLVAVGQFLICMLPYRSPFLHYALSAQPISTGVBSVYTWIGYFCFTSNPF 340
    |||:::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 228 REHKATYVTLAAVCAFTICMFPYTAFTAYRGLRQDDAINEVLEKIVLMLGYALSANLPIL 287

0Y 341 YGCLNRQIRGELSKQFVCFKPAPEEELRLPSREG---SIEENFLQ 383
    |||:::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 288 YALANRDEFTGYQQLFFC-----RLANRSHSTSLRSNASQ 323

```

RESULT 15  
US-09-030-582-13  
; Sequence 13, Application US/09030582  
; Patent No. 5904506

```

APPLICANT: SOPPETT, DANIEL R
TITLE OF INVENTION: ADRENERGIC RECEPTOR
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: Catella, Byrne, Bain, Gilfillan, Cecchi
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,582
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,568
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-324
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
OS-09-030-582-13

```

Query Match	14.7%	Score 340:	DB 2:	Length 359;
Best Local Similarity	28.0%	Pred. No. 3e-19;		
Matches 97; Conservative	57;	Mismatches 134;	Indels 58;	Gaps 9;

```

0Y      49  MLDLDAVAGNNAVMVIAKTPALRKFV--FVPHLCVLDAALTPMLAMSSSLFD 106
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      25  LAVILITVAGNNVVCCLAVGLNRRLRLNLTNCFEYLSIALITDLGLGLLPF---SAIYO 79
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      107 HAL---FGEVVCRLYELTFVSCFVSLATLSVAIVERYYVYVHMRREVMRTLGIVASVL 163
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      80  LSCWKSFGKFCNNTYTSIDWMLCPASTILNLFMISLDRIYCAWDLRPVLTVPYRAISL 139
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      164 VGWVWKAALAAASVPE--LGRVSMEEGAPS--VPKCSLQWMSHAACTQVYVFAVIELPL 220
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      140 VLIWVISTITLSELIHIGWMSNRNETSKGNHTTSCCKQVYN----EYVGLVDGIVFYFLP 194
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

Oy 221 LLLLLVYCSMFRRARAAAMHGGLPTWMEPRRRESLSRSRTMTSSCAPQTTTPKTF 280
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 195 LLIMQITFYRRIFKFAADQAKRINHNISSKWA-----TI 227

Oy 281 GGGKAAVLLVAVGQELLICWLPYPSFHLYAALSQPISTQGVESVYTWIGTCTSNPF 340
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 228 REHKATVYLAAMKAFIICMPPEYTAFAVYRGLRGDDAINEVLEAIYVLMGYANSALNPIL 287

Oy 341 YGCLNRQIRGELSPOVCFKPAPEDEELRLPSREG---STEENPLQ 383
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 288 YAAALNRDERTGTYQDLFC-----RLANRRSHKSTLSLSNSQ 323

```

Search completed: October 21, 2002, 16:09:46  
Job time : 19 secs



GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: October 21, 2002, 16:08:10 : Search time 21 Seconds

(without alignments)  
2063.633 Million cell updates/sec

Title: US-09-838-028-2

Perfect score: 2318  
Sequence: 1 MESSRPIPOSSGNSSTIGRVP.....SDIMSDYLRRAPASPRLES 451

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR-71:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	823	35.5	428	2	151087	G protein-coupled
2	351	15.1	358	2	JQ1278	histamine H2 recep
3	349.5	15.1	440	2	JC5520	serotonin receptor
4	349	15.1	359	2	A39008	histamine H2 recep
5	343	14.8	359	2	JC4120	histamine H2 recep
6	340	14.7	359	2	JH0449	histamine H2 recep
7	338.5	14.6	436	2	JN0591	serotonin receptor
8	337	14.5	400	2	A53281	beta-3-adrenergic
9	336	14.5	400	2	A41679	beta-3-adrenergic
10	335.5	14.5	405	2	S65459	beta-3-adrenergic
11	335	14.5	428	2	A55044	beta-4C-adrenergic
12	332.5	14.3	572	2	I39369	alpha-1A-adrenergic
13	329.5	14.2	437	2	I57942	5-hydroxytryptamin
14	326.5	14.1	400	2	S32804	beta-3-adrenergic
15	324	14.0	414	1	QRH083	beta-3-adrenergic
16	322.5	13.9	418	2	G02953	beta-3-adrenergic
17	322.5	13.9	560	2	A38731	alpha-1A adrenergic
18	320	13.8	501	2	JH0447	alpha-1A adrenergic
19	319.5	13.8	408	1	QRH086	beta-3-adrenergic
20	317.5	13.7	379	2	JC6178	serotonin receptor
21	308	13.3	517	2	A45121	alpha-1B adrenergic
22	305	13.2	515	2	A40491	alpha-1B adrenergic
23	300	12.9	429	2	S65656	alpha-1C-adrenergic
24	300	12.9	466	2	JN0765	alpha-1C-adrenergic
25	300	12.9	489	2	S65657	alpha-1C-adrenergic
26	292.5	12.6	564	2	A38271	alpha-1C-adrenergic
27	292	12.6	466	2	I57959	serotonin receptor
28	291.5	12.6	515	2	JC1525	alpha-1C adrenergic
29	291	12.6	477	2	S71323	alpha-1B-adrenergic

30	290.5	12.5	501	2	T18863	hypothetical prote
31	290	12.5	466	2	A35375	alpha-1-adrenergic
32	289.5	12.5	388	2	JN0605	somatosatin recep
33	285	12.3	446	1	DYH0D1	dopamine receptor
34	284.5	12.3	385	2	S68780	dopamine D1-like r
35	283	12.2	446	2	I47217	dopamine receptor
36	281.5	12.1	384	2	A47249	brain-specific som
37	278	12.0	459	2	A56849	dopamine receptor-
38	277.5	12.0	422	2	I38209	serotonin receptor
39	277.5	12.0	483	2	A25896	beta-adrenergic re
40	277.5	12.0	511	2	S44275	dopamine receptor
41	274	11.8	387	2	I49246	D4 dopamine recept
42	272	11.7	444	2	C55886	dopamine receptor
43	271.5	11.7	448	2	A47519	serotonin receptor
44	270.5	11.6	384	2	JC4629	somatosatin recep
45	270	11.6	402	2	I56595	neurokinin 2 recep

## ALIGNMENTS

## RESULT 1

I51087

G protein-coupled seven-transmembrane receptor - Japanese medaka

C:Species: Oryzias latipes (Japanese medaka)

C&gt;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000

C:Accession: I51087

R:Yasuoaka, A.; Abe, K.; Saigo, K.; Arai, S.; Emori, Y.

Biochim. Biophys. Acta 1235, 467-469, 1995

A:Title: Molecular cloning of a fish gene encoding a novel seven-transmembrane recept

A:Reference number: I51087; MWID:95275927

A:Accession: I51087

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-428 &lt;YAS&gt;

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

## Query Match

Best local similarity 42.3%; Pred. No. 3.6e-59;

Matches 184; Conservative 81; Mismatches 142; Indels 28; Gaps 11;

QY	2	ESSPI---POSSGNSST--LGRVQTPGPSTASVPEVGL-----RDVASSEVALFFMLL	52
DB	5	KTSPMTSDHSISNFTSGFGPHPTVP-----PDVGAVTSSQSQMKDLFGLECVTL	56
QY	53	DLTPVAGNAVMVAITAKTPALRKFEVFNHCLVDLLAALTMLPLMSSALFEDHALFGE	112
DB	57	NLTALLNTGVMVAIARAPHLKRFACVCHLCADVLCAILLPLGLITSSSPFCTVFTI	116
QY	113	VACRLVFLSCVFSVALISVSATINVERYYVHPMKREVMRLGLVAVLVGVWVAKALA	172
DB	117	LECGVYIFLNVFLWLSITLTAISVERFYVHPMKREVMRLGLVAVLVGVWVAKALA	176
QY	173	MASVPVGRVSWERGASVPPGCSLQWSHSAQCQLFFVFAVLFLPLLLILLVYCSMF	232
DB	177	LALVTLFGWPPYGHQSSIAASHCSLHSHSLRKLRCVFAVLCVCEFLAPVAVIFSISYAVY	236
QY	233	RVARVAMQGP--LPTWMT--PRORSESSSRSTWYSSGAPD--TPHRTFGGKAAYV	288
DB	237	KVASASALQGVPAVFTMAADSPAKRDSINSOTITTTTRTLTPORLSPEAFSGKALRT	296
QY	289	LAVGQFLLCWLDPYFSFHLHYVALSAQPISTGVESVVTWIGYFCFTSNPFYGLCKLRQI	348
DB	297	LAVTQGLVLCWLPDFYFHLQMSLTGSMKSPGDLAEAVNMVLASSFVAVNSFFGLNKRQI	356
QY	349	RGELSK-QFVCFKRPAREBELRLPSRGSTIEENFTLOLTGCGSSSEWVSRPLSPK-OE	406
DB	357	RDELVKKRRCCVTPV---EIGSSLEGSFOENFLQRTSSSETHPSFANSNPRNME	413
QY	407	PPAVDFRIQCIAGE 421	

Db 414 NQA--HKIPQIPPE 426

## RESULT 2

J01278

histamine H2 receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C&gt;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 05-Nov-1999

C:Accession: J01278

R:Rat, M.; Traiffort, E.; Arrang, J.M.; Leurs, R.; Schwartz, J.C.

Biochem. Biophys. Res. Commun. 179: 1470-1478, 1991

A:Title: Cloning and tissue expression of a rat histamine H2-receptor gene.

A:Reference number: J01278; MUID:92028890

A:Accession: J01278

A:Molecule type: DNA

A:Residues: 1-358 &lt;RNA&gt;

A:Cross-references: GB:S57565; NID:g236183; PIDN:AA819935.1; PID:g236184

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

F:22-45/Domain: transmembrane #status predicted &lt;TM1&gt;

F:58-81/Domain: transmembrane #status predicted &lt;TM2&gt;

F:93-113/Domain: transmembrane #status predicted &lt;TM3&gt;

F:116-159/Domain: transmembrane #status predicted &lt;TM4&gt;

F:178-203/Domain: transmembrane #status predicted &lt;TM5&gt;

F:224-260/Domain: transmembrane #status predicted &lt;TM6&gt;

F:267-288/Domain: transmembrane #status predicted &lt;TM7&gt;

F:4/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:220,311,315/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 15.1%; Score 351; DB 2; Length 358;

Best Local Similarity 27.5%; Pred. No. 6.3e-21;

Matches 106; Conservative 58; Mismatches 150; Indels 72; Gaps 12;

43 SVAFPMLLDLTAAGAAVAVIAKPRALRFV--FVPHCLVDLALTLPLMLLS 100

Db 22 SVLTTLTL--TIGAVVYCLAVSLNRLRLSLNCFIVSLAATDLGLVLPF-- 74

QY 101 SSALFDHAL--FGEVACRLVFLVCFVSLALSVAISAIINERYVYVHPRYEVMTIG 157

Db 75 -SAIQQLSTWFSFGHCNITVITSLDVMCTASILNFMISLDRCVAVTDPLRYVLPV 133

QY 158 LVASLVGVWKKALAMASVPLVGRVSE-----GAPSVPGCSLQMSHAYCOLFVV 211

Db 134 RVALSLVFIVVITSLTSLST--HLGWSNRNGTSGNDTFK--CKVOVN-----EYGLV 184

QY 212 FAVLYFLPLLLILVWVCSMFRAVAAHOGPLPTWMEPTROSESLSRSTWTSAGA 271

Db 185 DGLVTFPLPLIMCVYTRIKRIARQAKKRNHISMKAA----- 224

QY 272 PQTTPHRTFGGKAAYVLLAVGGFLCWLPRFSFHLVALSAQPISTGQVESVWTWIG 331

Db 225 -----TIREKATVTLAAVGAFFIICMPYFPAFVYRGLRDAINEAVEGIVLMIG 277

QY 332 FCFPSNPFYGCILNRQIRGELSKQVCFERK--APEELRL-----PSRESIENF 381

Db 278 ANSALNPLLYAALNRDFTAYQQLFHCKFASHSHKTSRLNLSLPRDSRGRMOBEK 337

QY 382 LQFLOGTCSPESWVSRPLPSKQEP 407

Db 338 PLKLD-----VMSCTELTHPGNP 356

## RESULT 3

JC5520

serotonin receptor 6 - human

N:Alternate names: 5-hydroxytryptamine receptor 6 (5-HT6)

C:Species: Homo sapiens (man)

C&gt;Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 05-Nov-1999

C:Accession: JC5520

R:Kohen, R.; Metcalf, M.A.; Khan, N.; Druck, T.; Huebner, K.; Lachowicz, J.E.; Meltzer, J.

A:Title: Cloning, characterization, and chromosomal localization of a human 5-HT 6 serot

A:Reference number: JC5520; MUID:96102917

A:Accession: JC5520

A:Molecule type: mRNA

A:Residues: 1-440 &lt;KOH&gt;

A:Cross-references: GB:L41147; NID:g1162923; PIDN:AA82622.1; PID:g1162924

A:Experimental source: brain

C:Comment: This protein shows high affinity for several therapeutically important ant

C:Genetics:

A:Gene: HTR6

A:Map position: 1p35-36

A:Introns: 238/3; 291/3

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tran

F:28-51/Domain: transmembrane #status predicted &lt;TM1&gt;

F:65-88/Domain: transmembrane #status predicted &lt;TM2&gt;

F:100-123/Domain: transmembrane #status predicted &lt;TM3&gt;

F:143-166/Domain: transmembrane #status predicted &lt;TM4&gt;

F:185-208/Domain: transmembrane #status predicted &lt;TM5&gt;

F:266-289/Domain: transmembrane #status predicted &lt;TM6&gt;

F:298-321/Domain: transmembrane #status predicted &lt;TM7&gt;

F:10/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.1%; Score 349.5; DB 2; Length 440;

Best Local Similarity 30.7%; Pred. No. 1e-20;

Matches 127; Conservative 59; Mismatches 171; Indels 57; Gaps 18;

QY 19 VPOTPGSTASGVEVGLRDVASES---VALPFMLLDLTAAGAAVAVIAKPRALR 74

Db 2 VPE-PGP-TNSTPRAMKAGPSAPGSGWVAALCVIALTA--AANSLIALICTOPALR 58

QY 75 KE--VEVPHCLVDLALTLPLAMLSALFPHALFGEVACRLVFLVCFVSLAIS 132

Db 59 NTSNFFLVSLFTSDLMGLVMPAPML--NALYGRWLARGLCLLWAFDMCCSASILN 116

QY 133 VSAINVERVYVHPRYEVMTIGLVASVLYGVWVAAALMASVPLVGRVSE--GAP 189

Db 117 LCLISLDRTLLSLPRLKRLMPLRLALVLAWSLAALASFLPL--IGMELGARP 174

QY 190 SVPPGCSLQMSHAYCOLFVVVFAVLYFLPLLLILVWVCSMFRAVAAHOGPLPTW 249

Db 175 PVPQCRLASLP-----FVLVAGLFLFPLSGAICFYCYRIILAKKQAVQVSLTGM 229

QY 250 -----ETPRQSESLSRSTWTSAGAQTTTPHRTFGGKAAYVLLAVGGFL 298

Db 230 ASQASETLQVPRTPPGESASRLATKHSKAL-----KASLTGLIGLMEFV 279

QY 299 CWLPYFSPHLVALSAQPISTGQVESVWTWIGYCFPSNPFYGCILNRQIRGELSKQFVC 358

Db 280 TWLPFFVANIYQAV--CCISIFGLD--VLTWIGYCNSTNMPITVLPFRDRALGR----- 333

QY 359 FFKPAPEELRLP--SRGSIENFLQFLOGTCSPESWVSRPLPSKQEP 411

Db 334 -FLPCP-----RCPRQASLASPLRLTSHSGRRGLS--LQGVLPRLP--PPSD 379

## RESULT 4

A39008

histamine H2 receptor - dog

C:Species: Canis lupus familiaris (dog)

C&gt;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 24-Nov-1999

C:Accession: A39008; A41821

R:Gantz, I.; Schaeffer, M.; DelValle, J.; Logsdon, C.; Campbell, V.; Uhler, M.; Yamad

Proc. Natl. Acad. Sci. U.S.A. 88: 429-433, 1991

A:Title: Molecular cloning of a gene encoding the histamine H2 receptor.

A:Reference number: A39008; MUID:9110543

A:Accession: A39008

A:Molecule type: DNA

A:Residues: 1-359 &lt;GAN&gt;

A:Cross-references: GB:342701; NID:g163951; PIDN:AA85637.1; PID:g163952

A:Note: the nucleotide sequence described in this paper has been revised; the amino a

submitted to the Protein Sequence Database, March 1992

A:Reference number: A41821

A:Accession: A41821

A:Molecule type: DNA  
A:Residues: 1-359 <GA2>  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 15.1%; Score 349; DB 2; Length 359;  
Best Local Similarity 28.7%; Pred. No. 9,2e-21;  
Matches 100; Conservative 56; Mismatches 140; Indels 52; Gaps 10;

OY 43 SVAFELMLDLTAVAGNAAMAVIAKTPALRKEV--FVPHLCVLDLALTLPLMLSSALFD 100  
DB 22 SVTLTVLTLI---TIAGNVVVCVAVGLNRLRLSLTNCFLVSLAIDLLGLLVLPF---- 74  
OY 101 SSALPDHAL---FGEVACRLYLFLSVCFVSLAILSVSAINVERRYVVVHPMKREYRMTLG 157  
DB 75 -SAFQOLSCRSFGKVFVFCVITSLDMVLCVTAISILNLFMSIDRCVAVDPLRYVLPV 133  
OY 158 LVASVGVVWVKALMASVPV-LGRVSWEEGAP--SVPGCSLQWSHSAVCOLFVVVFAY 214  
DB 134 RYAVSLVLIWVISITLSFLSHLGMNSRNETSSFNHTIPKCKVQVN-----LVYGLVDGL 188  
OY 215 LYFLPLLLILLVYCSMFRVARVAAHQGLPTMETPRQSESLSSSTWVTSSGAPOT 274  
DB 189 VFYPLPLVMCTIYYRIFKRIADQAKRIHMGSKRA----- 225  
OY 275 TPHTFEGGKAAVVLVAVGGQFLCWLPRYFSFLYVALSAQPISTGQVESVYTWIGYCF 334  
DB 226 ----TIGHKATVTLAAVAGAFICWPFYFVYRGKGDADINAEAEVAVVLMGLVANS 281  
OY 335 TSNPFYGCNLQINGELSKQVCFKPAPE--EELRLPSREGSTEEN 380  
DB 282 ALNPLVLTNLNDRFTAVQQLFRC--RPASHAQETSLRSNSQLARN 327

## RESULT 5

JC4120  
histamine H2 receptor - guinea pig  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 27-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 24-Nov-1999  
C:Accession: JC4120  
R:Traillfort, E.; Vizuete, M.L.; Tardivel-Lacombe, J.; Soull, E.; Schwartz, J.C.; Ruat, M.  
Biochem. Biophys. Res. Commun. 211, 570-577, 1995  
A:Title: The guinea pig histamine H2 receptor: gene cloning, tissue expression and chrom  
A:Reference number: JC4120; MUID:95314628  
A:Accession: JC4120  
A:Molecule type: DNA  
A:Residues: 1-359 <TRA>  
C:Comment: Histamine, a messenger molecule in cell-to-cell communication, affects its ta  
ly defined receptor subtypes named H1, H2 and H3.  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
F:22-45/Domain: transmembrane #status predicted <TM1>  
F:58-81/Domain: transmembrane #status predicted <TM3>  
F:93-113/Domain: transmembrane #status predicted <TM3>  
F:136-157/Domain: transmembrane #status predicted <TM4>  
F:179-204/Domain: transmembrane #status predicted <TM5>  
F:235-226/Domain: transmembrane #status predicted <TM6>  
F:269-289/Domain: transmembrane #status predicted <TM7>  
F:4,162,168/Binding site: carbohydrate (asn) (covalent) #status predicted  
F:221,316/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predict  
F:226,357/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predict

Query Match 14.8%; Score 343; DB 2; Length 359;  
Best Local Similarity 27.0%; Pred. No. 2,8e-20;  
Matches 99; Conservative 57; Mismatches 146; Indels 64; Gaps 11;

OY 49 MLLDLTAVAGNAAMAVIAKTPALRKEV--FVPHLCVLDLALTLPLMLSSALFD 106  
DB 25 LIILITLVAGNVVVCVAVGLNRLRLSLTNCFLVSLAIDLLGLLVLPF-----SAIQ 79  
OY 107 HAL---FGEVACRLYLFLSVCFVSLAILSVSAINVERRYVVVHPMKREYRMTLG 163  
DB 80 LSCKSFKVCNITSLDMVLCVTAISILNLFMSIDRCVAVDPLRYVLPVLTIPAVATSL 139

OY 164 VGVWVKALAMASVPVLAGRVSWEEGAPSVPG-----CSLQWSHSAVCOLFVVVFAYVLF 218  
DB 140 VFIWVISTLSLST--HLGWSNRNETSKNDNTYKCKVQVN-----EYGLVDGLVIFY 192

OY 219 LPLLILVYCSMFRVARVAAHQGLPTMETPRQSESLSSSTWVTSSGAPOTPHR 278  
DB 193 LPLLIMCTIYFRIKRIADQAKRIHMGSKRA----- 225

OY 279 TFGGKAADVLLAVGGQFLCWLPRYFSFLYVALSAQPISTGQVESVYTWIGYCF 338  
DB 226 TIREHKATVTLAAVAGAFICWPFYFVYRGKGDADINAEAEVAVVLMGLVANSALNP 285

OY 339 PFYGCNLQINGELSKQVCFKPAPEEELRLP---SREGSTEENFLOFLOCTGCPSESW 395  
DB 286 ILVYALNDRFTAVYHQLECC-----RLASHNSHETSLRLNNSQ-LNRSQCQEPBW 334

OY 396 -VSRPL 400  
DB 335 QEDKPL 340

## RESULT 6

JH0449  
histamine H2 receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 24-Nov-1999  
C:Accession: JH0449; I52319  
R:Gantz, I.; Munzert, G.; Tashiro, T.; Schaeffer, M.; Wang, L.; DelValle, J.; Yamada,  
Biochem. Biophys. Res. Commun. 178, 1386-1392, 1991  
A:Title: Molecular cloning of the human histamine H2 receptor.  
A:Reference number: JH0449; MUID:91337087  
A:Accession: JH0449

## A:Molecule type: DNA

A:Residues: 1-359 <GAN>  
A:Cross-references: GB:M64799; NID:g184087; PIDN:AA58647.1; PID:g184088  
R:Nishi, T.; Koike, T.; Oka, T.; Maeda, M.; Futai, M.  
Biochem. Biophys. Res. Commun. 210, 616-623, 1995  
A:Title: Identification of the promoter region of the human histamine H2-receptor gen  
A:Reference number: I52319; MUID:95275318  
A:Accession: I52319  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-359 <RES>  
A:Cross-references: GB:D49783; NID:g728495; PIDN:BA40818.1; PID:g728496  
C:Comment: Histamine is important in the regulation of gastric acid secretion.  
C:Genetics:  
A:Gene: GDB:HRH2  
A:Cross-references: GDB:391259; OMIM:142703

A:Map position: 5pter-5qter  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; transmembrane protein  
F:23-44/Domain: transmembrane #status predicted <TM1>  
F:58-81/Domain: transmembrane #status predicted <TM2>  
F:93-114/Domain: transmembrane #status predicted <TM3>  
F:135-159/Domain: transmembrane #status predicted <TM4>  
F:181-204/Domain: transmembrane #status predicted <TM5>  
F:233-258/Domain: transmembrane #status predicted <TM6>  
F:268-289/Domain: transmembrane #status predicted <TM7>

Query Match 14.7%; Score 340; DB 2; Length 359;  
Best Local Similarity 28.0%; Pred. No. 4,9e-20;  
Matches 97; Conservative 57; Mismatches 134; Indels 58; Gaps 9;

OY 49 MLLDLTAVAGNAAMAVIAKTPALRKEV--FVPHLCVLDLALTLPLMLSSALFD 106  
DB 25 LAVILITVAGNVVVCVAVGLNRLRLSLTNCFLVSLAIDLLGLLVLPF-----SAIQ 79  
OY 107 HAL---FGEVACRLYLFLSVCFVSLAILSVSAINVERRYVVVHPMKREYRMTLG 163  
DB 80 LSCKSFKVCNITSLDMVLCVTAISILNLFMSIDRCVAVDPLRYVLPVLTIPAVATSL 139  
OY 164 VGVWVKALAMASVPV-LGRVSWEEGAP--VPPGCSLQWSHSAVCOLFVVVFAYVLFLLP 220

Db 140 VLIWISTFLSLIHLGWNNSRNETSKGNHTTSKCKVOVN-----EYGLVDGLVTPLP 194  
OY 221 LLLLVVCSMRVARVAVAMOHGRLPTWMEPTPROSESLSNSTWTSAGAPQTPHRTF 280  
Db 195 LLIKITTYRIFKVRDKKRNHISMKAA-----TI 227  
OY 281 GGGKAAYVLLAVGGOLFCLMLPFPSFHLVVALSAOPISITGOVESVVTWIGYFCFTSNPFF 340  
Db 228 REHKATVTLAAVGAFTICMPFYAFYVYRGLRGDDALNEVLEALVLMGVANSLANPIL 287  
OY 341 YGCLNRQIRGELSKOPVCFKPAPEEELRLPSREG---SIENFIQ 383  
Db 288 YALNRDRERTGYQLFCC-----RLANRNSHKTSLRSNASQ 323

RESULT 7  
JN0591  
serotonin receptor 6 - rat  
N:Alternate names: 5-hydroxytryptamine receptor 6 (5-HT6)  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 05-Nov-1999  
C:Accession: JN0591  
R:Ruat, M.; Telford, E.; Arrang, J.M.; Tardivel-Iacombe, J.; Diaz, J.; Leurs, R.; Schw  
Biochem. Biophys. Res. Commun. 193, 268-276, 1993  
A:Title: A novel rat serotonin (5-HT6) receptor: molecular cloning, localization and st  
A:Reference number: JN0591; MUID:93277562  
A:Accession: JN0591  
A:Molecule type: DNA  
A:Residues: 1-436 <RUA>  
A:Cross-references: GB:S62043; NID:g385708; PIDN:AMB26908.1; PID:g385709  
C:Genetics:  
A:Introns: 238/3  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein  
F:29-53/Domain: transmembrane #status predicted <TM>  
F:63-84/Domain: transmembrane #status predicted <TM>  
F:95-122/Domain: transmembrane #status predicted <TM>  
F:141-168/Domain: transmembrane #status predicted <TM>  
F:185-213/Domain: transmembrane #status predicted <TM>  
F:267-293/Domain: transmembrane #status predicted <TM>  
F:297-319/Domain: transmembrane #status predicted <TM>  
F:9/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 14.6%; Score 338.5; DB 2; Length 436;  
Best Local Similarity 28.4%; Pred. No. 8.1e-20;  
Matches 129; Conservative 58; Mismatches 171; Indels 97; Gaps 20;

OY 2 ESSPIPOSSGNSSTLGRVPQTGPSTASGVPEVGLRDVASEVALFEMLLDLTVAGNA 61  
Db 4 EPGPV-----NSST---PAMGPGPPAPG-----GSGVVAALCVVIVLTA-AAANS 45  
OY 62 AVMAVIATKPALRKF--VFVPHLCVLDLALTLMLPLAMSSALFDHALFGEVACRYL 119  
Db 46 LLIIVLCIOPALRNTSNFVLVSLFSDLVAGLVMPPALV--NALGKRVLAGLCCLMT 103  
OY 120 FLVSCFVSLAISVAIINVERIYVYVHPMYEVRMTGLVASVLYGVWVKALAMASVPL 179  
Db 104 AFDVWCASSTINLCILISDRYLITLSPRLRYKRLMTAPRALALIGANSLAALASFLPL 163  
OY 180 GRVSWEE-GAPSV--PGCSLQMSHAYCOL-----FVVYFAVLFLPILLILLVYCSMF 232  
Db 164 -LGMHELGKARTPAPG-----QCRLASLPFVLVASVTFPLPSGALCFPTCRIL 212  
OY 233 RVARAANOHOGLPTWM-----ETPRQSESLSSRSTWVTSSGAPQTPPHRTF 281  
Db 213 LAARKQAOAVASLTGTGQALETLQVPTPRPGMESADSRRLATKHSKAL----- 264  
OY 282 GGAAVVLLAVGGOLFCLMLPFPSFHLVVALSAOPISITGOVESVVTWIGYFCFTSNPFF 341  
Db 265 -KASLTGILGMEFVWMLPFFVANIOAV-CDGISGLRP-VLTWIGYCSSTNPIIY 320  
OY 342 GCLNRQIRGELSKOPVCFKPAPEEELRLP-----SREGSI 377

Db 321 PLFMRDFKRALGRELPCVHC-PEHRPALPPPGCLTAVPDQASACSRCCCLCRLQOI 379  
OY 378 EENFIQFLOGT--GC---PSESWSRPLPSPKQEP 407  
Db 380 QTP-----LQGAPRACSSQPSFCCLERPPGTPRHPP 410

RESULT 8  
A53281  
beta 3-adrenergic receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 13-Aug-1999  
C:Accession: A53281; S29808  
R:Graneman, J.G.; Lahners, K.N.; Chaudhry, A.  
Mol. Pharmacol. 40, 895-899, 1991  
A:Title: Molecular cloning and expression of the rat beta 3-adrenergic receptor.  
A:Reference number: A53281; MUID:92100057  
A:Accession: A53281  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-400 <GRA>  
A:Cross-references: GB:S73473; NID:g241215; PIDN:AMB20702.1; PID:g241216  
A:Note: sequence extracted from NCBI backbone (NCBIN:73473, NCBI:P:73476)  
R:Bensaid, M.; Kaghad, M.; Rodriguez, M.; le Fur, G.; Caput, D.  
FEBS Lett. 318, 223-226, 1993  
A:Title: The rat beta3-adrenergic receptor gene contains an intron.  
A:Reference number: S29808; MUID:93178631  
A:Accession: S29808  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-400 <BEN>  
A:Cross-references: GB:S56481; NID:g298306; PIDN:AMB25520.1; PID:g298307  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 14.5%; Score 337; DB 2; Length 400;  
Best Local Similarity 28.2%; Pred. No. 9.7e-20;  
Matches 120; Conservative 65; Mismatches 188; Indels 52; Gaps 17;

OY 4 SPIPOSSGNSSTLGRVPQTGPSTASGVPEVGLRDVASEVALFEMLLDLTVAGNA 62  
Db 2 APWPKNSGLFWSDAPPLDPSAANTSGLPV-----PMAALAGALLALATVAGML 54  
OY 63 VMAYIAKTPALRKF--VFVPHLCVLDLALTLMLPLAMSSALFDHALFGEVACRYL 120  
Db 55 VITALARTPRIGOTINVTSLATADLVVGLVMPG--ATLALGHPPLGATGCELMTS 112  
OY 121 LSVCFVSLAISVAIINVERIYVYVHPMYEVRMTGLVASVLYGVWVKALAMASVPL 180  
Db 113 VDVLCTVTAISIEFLCALAVDRYLAVTNPLRYGLTKRRARAAYVWIVASATVSFAPIMS 172  
OY 181 RVSWE GAPSVPGCSLQMSHAYCOL-----FVVYFAVLFLPILLILLVYCSMFVA 235  
Db 173 Q-WMRVGADEAQECH---SNPRCCSFASNMPTALSSVSFYLDLVLMLVYARVYVA 228  
OY 236 ---FVAAMOHGRLPTWMEPT--ORSESLSSRSTWVTSSGAPQ--TTPHR--TFGGKA 285  
Db 229 KRORRLRLRELGRPP--DESPRSRSPSPATVGPPTASDGVSGRRPARLLPLGEHRA 287  
OY 286 AVLLAVGGOLFCLMLPFPSFHLVVALSAOPISITGOVESVVTWIGYFCFTSNPFFGCLN 345  
Db 288 LRTLLINGISFLCPLPFLANVLRALGPSLVPSGVFTALNWLGYANSAFNPLIY-CRS 346  
OY 346 ROIIGELSKOPVCFKPAPEEELR-----LPSREGSIENFIQILOGGCPSESVS 397  
Db 347 PDER-DAFRRLDCSYGGNGPEEPVYTPPASPASRONSPLNRF-----DGYEGE----- 395  
OY 398 RPLPS 402  
Db 396 RPPPT 400



## RESULT 9

A1679

beta-3-adrenergic receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 13-Aug-1999

C:Accession: A1679

R:Muzzin, P.; Revelli, J.P.; Kuhne, F.; Cocayne, J.D.; McCombie, W.R.; Venter, J.C.; Gia

R: Biol. Chem. 266, 24053-24058, 1991

A:Title: An adipose tissue-specific beta-adrenergic receptor. Molecular cloning and down

A:Reference number: A1679; MUID:92084710

A:Accession: A1679

A:Molecule type: mRNA

A:Residues: 1-400 &lt;MU2&gt;

A:Cross-references: GB:M74716; NID:9950087; PIDN:AAA4470.1; PID:g202766

A:Experimental source: brown adipose tissue

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

F:8/26/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 28.2%; Pred. No. 1.2e-19; Length 400;

Matches 120; Conservative 64; Mismatches 189; Indels 52; Gaps 17;

QY 4 SPIQSSGNSSTLGRVPO--TRGPSTASGVPEVGLRDVASSEVALFFMLLDLTAVAGNNA 62

Db 2 APWPHKNSLAFWSDAPFLDPSAANTSGIPGV-----PMAALAGALLALATVGNL 54

QY 63 VMAVIAKTPALRK--VVVFHLCLVDLALTLMPMLSSALFDHALFGEACRYLF 120

Db 55 VITALARTPRLOTINNVETSLATADLVVGLVMPG--ATLALGHPMLGTGCELWTS 112

QY 121 LSVCFVSLATLSVAINVERYYVHPMKRYEVRMTGLVASVYGVWVKALAMASVPVIG 180

Db 113 VDVLCTVTSIETLCALAVDRILATNPLRYGLTKRRARAVALVWVVASVATVPATMS 172

QY 181 RVSWEGASVPYPGCSLQMSHAYCOL-----FVVFAVLYFLDLLILVYCMFRYA 235

Db 173 Q-WMVVGADAEQGECH---SNPRCSFASNMRYALLSSVSRYLPVLVLPYARVYVA 228

QY 236 ----RVAAMOHGPLETMMETPR--ORSELSRSSTWVTSSGAP--TTPHR--TFGGKA 285

Db 229 KRORFVRRELGRPP--EESPRSPSPSPATVGTPTASDGVSCRRPARLLPGEHRA 287

QY 286 AVLLAVAGGOFLLCWLPRFSEHLYVALSAOPISITQVESVWVWIGYFCFTSPFFYGLN 345

Db 288 LRTGLIGTISLCLWLPFLAVLALVPSLVPSGVFTALWLDGANSAPPLIY-CRS 346

QY 346 ROIRGELSKQVCFKPAPEEELR-----LPSREGSIEENFLQFLOGTGPSESWVS 397

Db 347 PDFR-DARFRLLCSYGGGPEEPVYVTFPASPVASRQNSPLNRF-----DQYEGE---- 395

QY 398 RPLPS 402

Db 396 RPFPT 400

## RESULT 10

S65459

beta-3-adrenergic receptor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Aug-1999

C:Accession: S65459

R:Pietri-Rouxel, F.; Lenzen, G.; Kapoor, A.; Dymare, M.F.; Archimbault, P.; Strosberg,

Eur. J. Biochem. 230, 350-358, 1995

A:Title: Molecular cloning and pharmacological characterization of the bovine beta3-adre

A:Reference number: S65459; MUID:95324546

A:Accession: S65459

A:Molecule type: mRNA

A:Residues: 1-405 &lt;PIE&gt;

A:Cross-references: EMBL:X85961; NID:9757758; PIDN:CAAS9937.1; PID:9757759

A:Experimental source: brown adipose tissue

R:Castella, L.; Muzzin, P.; Revelli, J.P.; Riquier, D.; Giacobino, J.P.

Biochem. J. 297, 93-97, 1994

A:Title: Expression of beta(1) - and beta(3) -adrenergic-receptor messages and adenylat

ite fat.

A:Reference number: S40503; MUID:94107292

A:Accession: S40504

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 162-298 &lt;CAS&gt;

R:Stoffel, B.; Meyer, H.H.D.

submitted to the EMBL Data Library, June 1992

A:Description: Bovine beta3-adrenergic receptor, partial genomic sequence.

A:Reference number: S31659

A:Accession: S31659

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 4-5, 'HE', 8-105 &lt;STO&gt;

A:Cross-references: EMBL:X67214

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tran

F:37-63/Domain: transmembrane #status predicted &lt;TM2&gt;

F:73-101/Domain: transmembrane #status predicted &lt;TM2&gt;

F:113-133/Domain: transmembrane #status predicted &lt;TM3&gt;

F:156-179/Domain: transmembrane #status predicted &lt;TM4&gt;

F:204-225/Domain: transmembrane #status predicted &lt;TM5&gt;

F:293-314/Domain: transmembrane #status predicted &lt;TM6&gt;

F:327-347/Domain: transmembrane #status predicted &lt;TM7&gt;

F:8/26/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 28.1%; Pred. No. 1.3e-19; Length 405;

Matches 121; Conservative 67; Mismatches 183; Indels 59; Gaps 18;

QY 7 PQSSGNSSTLGRVPTP--GPST--ASGVPEVGLRDVASSEVALFFMLLDLTAVAGNNA 62

Db 3 PWPBPNSS-LTPWPDIPFLAPYATANASGIPGVW---AVALAGALLALATVATVGNL 57

QY 63 VMAVIAKTPALRK--VVVFHLCLVDLALTLMPMLSSALFDHALFGEACRYLF 120

Db 58 VITALARTPRLOTINNVETSLATADLVVGLVMPG--ATLALGHPMLGTGCELWTS 115

QY 121 LSVCFVSLATLSVAINVERYYVHPMKRYEVRMTGLVASVYGVWVKALAMASVPVIG 180

Db 116 VDVLCTVTSIETLCALAVDRILATNPLRYGLTKRRALAVALVWVVASVATVPATMS 175

QY 181 RVSWEGASVPYPGCSLQMSHAYCOL-----FVVFAVLYFLDLLILVYCMFRYA 235

Db 176 K-WMVVGADAEQGECH---SNPRCSFASNMRYALLSSVSRYLPVLVLPYARVYVA 231

QY 236 ----RVAAMOHGPLETMMETPR--ORSELSRSSTWVTSSGAP--TTPHRTFGGG 283

Db 232 TROLRLRELGRFPPEESPAPRSRSGSLAGPCASAGVSYRRARLLPLREH--- 288

QY 284 KAAVLLAVGQFLLCWLPRFSEHLYVALSAOPISITQVESVWVWIGYFCFTSPFFYGC 343

Db 289 RALRTGLIGTISLCLWLPFLAVLALVPSLVPSGVFTALWLDGANSAPPLIY-C 347

QY 344 LNRQIRGELSKQVCFKPAPEEELR--PSREGSIEENFLQFLOGTGPSESWSRPL 401

Db 348 RSPDFRSAP-RRLDC--RCRPEEHLAASPPR-----APSCAPALTATSP 388

QY 402 SPKQEPYAVD 411

Db 389 AGPMQPPELD 398

## RESULT 11

A55044

beta-4C-adrenergic receptor - turkey

C:Species: Meleagris gallopavo (common turkey)

C:Date: 18-Nov-1994 #sequence\_revision 18-Nov-1994 #text\_change 13-Aug-1999

C:Accession: A55044

R:Chen, X.; Harden, T.K.; Nicholas, R.A.

J. Biol. Chem. 269, 24810-24819, 1994

A:Title: Molecular cloning and characterization of a novel beta-adrenergic receptor.

A:Reference number: A55044; MUID:95014249  
A:Accession: A55044  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-428 <CH>  
C:Cross-references: GB:U13978; NID:g555881; PID:AAA62151.1; PID:g555882  
C:Genetics:  
A:Introns: 416/2  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: neurotransmitter receptor; transmembrane protein

Query Match                      14.5%; Score 335; DB 2; Length 428;  
Best Local Similarity    27.3%; Pred. No.1.5e-19;  
Matches    115; Conservative    59; Mismatches    179; Indels    68; Gaps    15;

```
OY      22 TPQSTASGVPEVGLRDVASSESVALFFMLLD-LTAVAGNAVMVIAKTPALRKF--VF 78
    ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
DB     2 TPLPANGSVPCNSMAVAIISRQMAVGALISTILIVVGNLLVIYAIAKTPTLQTMTNVF 61
OY      79 VEHCLVDLIAALTLMPLAMSSSALFDHALGEVACRYLFELSCFVSIALISAINV 138
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB     62 VTSLACADLVKGLLVPPG--ATILLGHMPYGTVCCELMSLDVLCTVASIEFLCAIAY 119
OY     139 ERYVVVHPMRREVMTGLVASVLGVWVKALMASVPVLGRVSMEGAPSVPGCSIQ 198
    ::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
DB     120 DRYLAITPALOYEALVTGKRAMAVCYMWAISAFISFLDIMH-WMRGDAEQAVRC--- 175
OY     199 WSHSAVYCOL-----EVVVEFAVLFLPLLILLVYCSEMFVA-----RVAAHQHG 243
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB     176 YDPRPCDDPVNTMMTVAIYSSTVSPFYVPLLVMIFVVRFAVATRIVQLGKKVRFLEEN 235
OY     244 PLPTMMEPTRPROSESLSNSTWTWSGAPQTTPHRTFG--GGKAIVLLAVGGOLFCLYL 301
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB     236 P-----SLSSK-----GGRMRPSRLLAIKERKALKTKIGIIWGTEFLCWL 275
OY     302 PFESHLVVALSAOPISIQVESVVTWIGYFCFTSNPFYCGLRNQINGELSKQEFVCFEK 361
    ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
DB     276 PEFFVANI-TKYECRLPVQDLFLFLNLGLGYNSANRPITY-CRSDFPSAEFKLLCC--- 330
OY     362 PAPEBELRLPREGSIIEENFLQFLQGTCGPSESWSRPLSPKQEPSPVDFRRIPQIAEE 421
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB     331 -----PRADRRLHAAPQDPQHSC-----AFSPRGDMDEDSKAVD---PEHLRED 373
OY      422 T 422
DB      374 S 374
```

RESULT 12

I39369

alpha-1a-adrenergic receptor - human

C:Species: Homo sapiens (man)

C:Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 13-Aug-1999

C:Accession: I39369; JC2331

R:Espenshade, T.A.; Hiratawa, A.; Tsujimoto, G.; Tanaka, T.; Yano, J.; Minneman, K.P.; Rabinowitz, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.; Blochem. Biophys. Res. Commun. 201, 1286-1304, 1994

A>Title: Cloning, expression and characterization of human alpha adrenergic receptors at

A:Reference number: JC2331; MUID:94296402

A:Accession: JC2331

A:Molecule type: mRNA

A:Residues: 1-30 'G' 32-521, 'P' 523-572 <WEI>

A>Note: The authors translated the codon CCC for residue 522 as Arg

C:Genetics:

A:Gene: GDB:ADRA1A; ADRA1; ADRA1R

A:Cross-references: GDB:118749; OMIM:104229  
A:Map position: 20pter-20qter  
A:introns: 37/3  
C:Superfamily: vertebrate rhodopsin C  
C:Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein  
F:89-123/Domain: transmembrane #status predicted <TM1>  
F:132-162/Domain: transmembrane #status predicted <TM2>  
F:172-197/Domain: transmembrane #status predicted <TM3>  
F:208-233/Domain: transmembrane #status predicted <TM4>  
F:254-278/Domain: transmembrane #status predicted <TM5>  
F:344-374/Domain: transmembrane #status predicted <TM6>  
F:380-414/Domain: transmembrane #status predicted <TM7>  
F:65,82/binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.3%; Score 332.5; DB 2; Length 572;  
Best Local Similarity 24.2%; Pred. No. 3,3e-19;  
Matches 122; Conservative 77; Mismatches 204; Indels 101; Gaps 16;

Qy 12 NSSTGLGRVQTPEPSPASGVPEYGLRDVASESAL-FPHLLDITLVAGAAVMVIATK 70  
| | | | | : | | | | | : | | | | | : |  
Db 65 NRSAGEPSGAGAGGDVNETAAVGGLVSAQGVSVPFLAAILMVAAGLVLIVLSACN 124  
  
Qy 71 PALRRFV--FPHLCVDLTALAALTPLMLSSALFDHALGECVACRLYLFLSYCFVSL 128  
| | | | | - | | | | | : | | | | | : | | | | | : |  
Db 125 RHLOQTNTFYIWLAVADLLISATVLPFS--ATMEVLGFMAFGRAFCDWMAADVLCCTA 182  
  
Qy 129 AILVSAINVERYYVHHPRVEVRMTGLVASVLGVWKALAMASVPYLGRVSMEEGA 188  
| | | | | : | | | | | : | | | | | : | | | | | : |  
Db 183 SILSLCTISVDRYVGVRHSIKYPALITERKAAILALLWVALVSVGPLG---WKE-- 237  
  
Qy 189 PSVPPECSIQWSHSAVCOL----FYVFAYVLFTPLRLLILTVYCSMPFVAR--VAAAG 241  
| | | | | : | | | | | : | | | | | : | | | | | : |  
Db 238 -PVPP-----DERCGITEAGYAVFSSVCEFYPMATIVMYCYRVVAVARSTRSLE 289  
  
Qy 242 HGPFLTWMETPROSE-----LSRSTWVTSSGA--POTTHPRFFGG----- 283  
  
Db 290 AG-----VKRRKGASEVLRIRHGCAATGADGHGHRSAAGHTFRSLSVRLKFSR 342  
  
Qy 284 --KAAVLLAVGGQILLCLPYFSPHLVVALSAQPISTGOVESVTWIGYFCETSNPFEY 341  
  
Db 343 EKKAATTLAIIVGVFIWCPFPFFVLPLGSLFPQLKPSEGFKVIFWLGTFNSCVNPLYI 402  
  
Qy 342 GCINRIKRGELSKQFPCFR-----PAPEELRLPSRESIDENLQPL 385  
| | | | | : | | | | | : | | | | | : | | | | | : |  
Db 403 PCSSRFFKRAFLILLRCQCRRRRRRLMRVYGHHMRASTGLROCAPSS----- 453  
  
Qy 386 OGTCGESESWSRPLRPKOEPRV-----DFRIPGOIAEETSEPLE 427  
| | | | | : | | | | | : | | | | | : | | | | | : |  
Db 454 -GDAPGARPALTALTDPDPEPGTPGMQAPVASRKPKPSAFKEMRLGLGFRPPTT---- 508  
  
Qy 428 QOULTSDIIMSYSYLPRPASPRLES 451  
| | | | | : | | | | | : | | | | | : | | | | | : |  
Db 509 -QLRAKVSSLSHKIRAGAQAARA 531

RESULT 13  
157942  
5-hydroxytryptamine receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I57942  
R:Monsma, F.J.  
Mol. Pharmacol. 43, 320-327, 1993  
A>Title: Cloning and expression of a novel serotonin receptor with high affinity for  
A:Reference number: I57942; MUID:93196608  
A:Accession: I57942  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-437 <RES>  
A:Cross-references: GB:I03202; NID:g294507; PIDN:AAA0618.1; PID:g294508  
C:Superfamily: vertebrate Rhodopsin

Query Match 14.2%; Score 329.5; DB 2; Length 437;

Query Match	14.1%	Score 326.5	DB 2	Length 400:
Best Local Similarity	27.4%	Pred. No. 6.9e-19;		
Matches 107;	Conservative 61;	Mismatches 171;	Indels 51;	Gaps 12;
F:201-222/Domain: transmembrane	#status predicted	<TM5>		
F:290-311/Domain: transmembrane	#status predicted	<TM6>		
F:324-344/Domain: transmembrane	#status predicted	<TM7>		
F:8,26/Binding site: carbohydrate (Asn)	(covalent)	#status predicted		
4 SPIPSSGNSSLGRVQ-TGPGSTASGVPEVGLRDVASSEVALFPMILLDTTAAVGNA	62			
2 AWPPIHNSGLAAMDAPILDPSSAANTGLGV-----PMAALAGALLATATYGGNLL	54			
63 VNAVIATKPALEKRF--VEVFHLCIYDLDAALMLPLMLSSSLDFHAGLEVACRLYDF	120			
55 VILAIARPRRLQTTINVFSTLAADLVYGLLVMPRG--ATLALGNHMPGLGTGELMTWS	112			
121 LSVCFYSLAITSVANVERYYVYVHPMKYEVRKMLGLVASLVGVGWKALAMASVPLVG	180			
113 YDVLCTVTSIETFLCALADRYLAVNPRLRYGTLTKRRARAIVVYLVIVSAVSEAPRMS	172			
181 RVSWEAGASVPVPGSGLOMSHSAYQOL-----FVVVFALYFLPRLPLLILVYVCSFRA	235			
173 Q-WMRVGADAEQOECH---SNPRCCSFMSNMRYALISSVSEFYLPYLWALFVARFVYA	228			
236 -----RVAMQHGRLPTTMMETPRQRSESLSRSTVYSSGAP-----QITTP	276			
229 KQRHLLRRELGRFPEDESPSPS-----RSPERATGCTPAAADGVPCGRRPARLLP	281			
277 HRTFGGKAAYVLLVAGGQFLLCMLPYPSFHLVYALSAOISTGVGVSVYTWIGYFCPTS	336			
283 LREH---RLRLTGLIGMGIFCSLWLPFFLALRALAGSLVPSGVFTALNMLGYANSAP	338			
337 NPEFYGCLNROIGELSKOYFCFFPAPPE	366			

```

RESULT 15
ORHUB3
beta-3-adrenergic receptor, splice form 2 - human
N:Alternate names: beta-3-adrenergic receptor form A
N:Contents: beta-3-adrenergic receptor splice form 1
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 18-Aug-1995 #text_change 16-Jun-2000
C:Accession: A11348; S33752
R:Emorine, L.J.; Marullo, S.; Briend-Sutren, M.M.; Patey, G.; Delavier-Klutt
Science 245, 1118-1121, 1989
A:Title: Molecular characterization of the human beta-3-adrenergic receptor.
A:Reference number: A11348; MUID:89368947
A:Accession: A11348
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-402 <EMO>
A:Cross-references: GB:M29932; NID:g178895; PIDN:AAA35550.1; PID:g178896
A:Note: splice form 1
R:Liellias, J.M.; Kaghed, M.; Rodriguez, M.; Chalou, P.; Bonnin, J.; Dupre, I.; Delpech
FEBS Lett. 324, 127-130, 1993
A:Title: Molecular cloning of a human beta-3-adrenergic receptor cDNA.
A:Reference number: S33751; MUID:93285320
A:Accession: S33752
A:Molecule type: DNA
A:Residues: 392-414 <LEU>
A:Cross-references: EMBL:X70812; NID:g312398; PIDN:CAA50142.1; PID:g1666375
A:Note: splice form 2
C:Genetics:
A:Gene: GDB:ADRB3
A:Cross-references: GDB:Z03869; OMIM:109691
A:Map position: 8p12-8p11.1
A:Introns: 402/2
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembr
F1-114/Product: beta-3-adrenergic receptor precursor splice form 2 #status predicted

```

F:1-402/Product: beta-3-adrenergic receptor precursor splice form 1 #status predicted <M  
F:37-63/Domain: transmembrane #status predicted <TM1>  
F:73-101/Domain: transmembrane #status predicted <TM2>  
F:113-133/Domain: transmembrane #status predicted <TM3>  
F:156-178/Domain: transmembrane #status predicted <TM4>  
F:204-225/Domain: transmembrane #status predicted <TM5>  
F:293-314/Domain: transmembrane #status predicted <TM6>  
F:327-347/Domain: transmembrane #status predicted <TM7>  
F:8,26/Blinding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.0%; Score 324; DB 1; Length 414;  
Best Local Similarity 28.7%; Pred. No. 1,1e-18;

Matches 125; Conservative 63; Mismatches 187; Indels 60; Gaps 21;

DB 4 SPIPSSGSSSTLGRVPPQPP--GPSNA--SGVEYGLRDVASESVALLFMLLDLTAVAG 59  
2 ARMPH---ENSSLAMPDLPTLPTANTSGLPVPW---EALALGALLALAVLATVGG 54  
QY 60 NAAVAVIAKTPALRK--VEVHLCVLDLALATLMLPLMLSSSLFEDHALFEVACRL 117  
DB 55 NLVIVAIAMTPTRLQTMVTFVTSIAADLVGMLVPPA--ATLALTGHPMLGATGCEL 112  
QY 118 YFLSVCEYSIALISVSAINVERIYVHPMYEVAMTIGLVA SVLVGVYKALAMASVP 177  
DB 113 WTSVDVLCVTASIEITLCALAVDRYLAVTNPLRYGALVTRCARTAVLVWVYSAVSEFAP 172  
QY 178 VLGRVSMEEGASVPPGCSLQMSHAYCOL----FVVVFAYLVFLPLLLILVYCSMF 232  
DB 173 IMSQ--WNRGALAEARORCH---SNPRCCAFASNMPIYLLSSVSFTPLLVMLFYIARVF 228  
QY 233 RVA---RVAAMQHGPPLPTMETPRORSELSR--STWVTSSGAP-----QTTPHRT 279  
DB 229 VVATRLRLRLRGELGRFP--EESPAPSRSLAPAPVGTCAPEGVACGRPARLLPRE 287  
QY 280 FCGGKAAYVLLVAVGQFLLCMIPYFSFLVYALSAPISTGQVESVYTIIGYFCFTSNPF 339  
DB 288 H--RALCTGLIMGFTLCLMPLFELANVLRALGGPSLVPGPAFLALNMLGYANSAFNPL 344  
QY 340 FYGCLNROIIGELSKQFVC---FFKPAPPEELR--LPS-----REGSIENFLOFLOG 387  
DB 345 IY-CRSPDERSAF--RLLCRCRCRRLPPEPCAAARPALFPSSGVPAAARSSPAQPRLCORLDG 402  
QY 388 -TGCPSESWSRPLP 401  
DB 403 FDSGCGEN---PLP 413

Search completed: October 21, 2002, 16:08:41  
Job time : 23 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:08:11 : Search time 14 Seconds  
(Without alignments)  
1247.323 Million cell updates/sec

Title: US-09-838-028-2

Perfect score: 2318  
Sequence: 1 MESSPIPOSSGNSSTIGRPV.....SDLIIMSDYLPRASPRLLES 451.

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	823	35.5	428	1	GPX1178 Oryzias lat
2	351	15.1	358	1	HH2R_RAT
3	349.5	15.1	440	1	SH6_HUMAN
4	349	15.1	359	1	HH2R_CANFA
5	345	14.9	358	1	HH2R_MOUSE
6	345	14.9	576	1	ALAD_RABIT
7	344	14.8	440	1	SH6_MOUSE
8	343	14.8	359	1	HH2R_CAVPO
9	340	14.7	359	1	HH2R_HUMAN
10	338.5	14.6	436	1	SH6_RAT
11	337	14.5	400	1	B3AR_RAT
12	335.5	14.5	405	1	B3AR_BOVIN
13	335.5	14.5	561	1	ALAD_RAT
14	335	14.5	428	1	B4AR_MELGA
15	332.5	14.3	572	1	ALAD_HUMAN
16	326.5	14.1	400	1	B3AR_MOUSE
17	323.5	14.0	405	1	B3AR_CAPIH
18	322.5	13.9	418	1	B3AR_MACMU
19	321.5	13.9	398	1	B3AR_FELCA
20	321.5	13.9	405	1	B3AR_SHEEP
21	320.5	13.8	562	1	ALAD_MOUSE
22	319.5	13.8	408	1	B3AR_HUMAN
23	317.5	13.7	379	1	GRE2_BALAM
24	315	13.6	351	1	B3AR_CAVPO
25	312.5	13.5	405	1	B3AR_CANFA
26	306.5	13.2	519	1	ALAB_HUMAN
27	305	13.2	515	1	ALAB_MESAU
28	301	13.0	515	1	ALAB_RAT
29	300.5	13.0	466	1	ALAA_CAVPO
30	300	12.9	466	1	ALAA_HUMAN
31	299.5	12.9	539	1	DOP2_DROME
32	298.5	12.9	466	1	ALAA_RABIT
33	295.5	12.7	514	1	ALAB_MOUSE

34	293.5	12.7	478	1	OPN4_HUMAN	Oguth6 homo sapien
35	292	12.6	466	1	ALAA_RAT	P43140 rattus norv
36	291.5	12.6	388	1	SH4_HUMAN	Q13639 homo sapien
37	291	12.6	470	1	ALAA_ORYLA	Q91175 Oryzias lat
38	290.5	12.5	501	1	YONJ_CABEL	O02213 caenorhabdi
39	290	12.5	466	1	ALAA_BOVIN	P18130 bos taurus
40	289.5	12.5	388	1	SSR4_HUMAN	P11391 homo sapien
41	289	12.5	446	1	DADR_MACMU	O77680 macaca mula
42	288	12.4	452	1	A2AA_BOVIN	Q28838 bos taurus
43	286.5	12.4	388	1	SH4_CAVPO	O70528 cavia porce
44	285.5	12.3	564	1	SH11_DROME	P20905 drosophila
45	285	12.3	446	1	DADR_HUMAN	P21728 homo sapien

## ALIGNMENTS

RESULT 1	ID	GPX1178	STANDARD	PRT	428 AA.
AC	Q91178				
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	01-NOV-1997	(Rel. 35, Last annotation update)			
DE	Probable G protein-coupled receptor (Fragment).				
OS	Oryzias latipes (Medaka fish).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;				
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;				
OC	Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.				
OX	NCBI_TaxID=8090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=95275927; PubMed=7756357;				
RA	Yasuoka A., Abe K., Saigo K., Arai S., Emori Y.;				
RT	"Molecular cloning of a fish gene encoding a novel				
RT	seven-transmembrane receptor related distantly to catecholamine,				
RT	histamine, and serotonin receptors.";				
RL	Biochim. Biophys. Acta 1235:467-469(1995).				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	-----				
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CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	-----				
DR	EMBL: DA3633; BAA07741.1; -.				
DR	GCRDB: GCR_1566; -.				
DR	InterPro: IPR00276; GPCR_Rhodpsn.				
DR	Pfam: PF00001; 7tm_1; 1.				
DR	PROSITE: PS00237; G-PROTEIN RECP_F1_1; 1.				
DR	PROSITE: PS50262; G-PROTEIN RECP_F1_2; 1.				
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.				
FT	DOMAIN 1				
FT	TRANSMEM 47				
FT	TRANSMEM 68				
FT	DOMAIN 94				
FT	TRANSMEM 115				
FT	DOMAIN 121				
FT	TRANSMEM 141				
FT	DOMAIN 142				
FT	TRANSMEM 163				
FT	DOMAIN 184				
FT	TRANSMEM 211				
FT	DOMAIN 232				
FT	TRANSMEM 294				
FT	DOMAIN 315				
FT	DOMAIN 395				
FT	CARBOHYD 18				
FT	NON_TER 428				



DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 5-hydroxytryptamine 6 receptor (5-HT<sub>6</sub>) (Serotonin receptor).  
 GN HTR6.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 NC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Striatum;  
 RX MEDLINE=96102917; PubMed=8522988;  
 RA Kohen R., Metcalf M.A., Khan N., Druck T., Huebner K., Lachowicz J.E.,  
 RA Sibley D.R., Roth B., Hamblin M.W.;  
 RT "Cloning, characterization, and chromosomal localization of a human  
 RT 5-HT<sub>6</sub> serotonin receptor.";  
 RL J. Neurochem. 66:47-56(1996).  
 RN [2]  
 RP SEQUENCE OF 215-280 FROM N.A.  
 RC TISSUE=Striatum;  
 RX MEDLINE=95385798; PubMed=7656980;  
 RA Ullmer C., Schumack K., Kalkman H.O., Lubbert H.;  
 RT "Expression of serotonin receptor mRNAs in blood vessels.";  
 RL FEBS Lett. 370:215-221(1995).  
 CC -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR  
 CC 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS  
 CC AS A NEUROTANSMITTER. A HORMONE, AND A MITOGEN. THE ACTIVITY OF  
 CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE  
 CC CYCLASE. IT HAS A HIGH AFFINITY FOR TRICYCLIC PSYCHOTROPIC DRUGS.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN SEVERAL HUMAN BRAIN REGIONS, MOST  
 CC PROMINENTLY IN THE CAUDATE NUCLEUS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: LA1147; AAA92622.1; -;  
 DR EMBL: Z49119; CA88929.1; -;  
 DR GCRDB: GCR\_1062; -;  
 DR GCRDB: GCR\_1885; -;  
 DR MIM: 601109; -;  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PRO1102; 5HT6RECEPT.  
 DR PROSITE: PS00237; G.PROTEIN\_RECPT\_FL\_1; 1.  
 DR PROSITE: PS50262; G.PROTEIN\_RECPT\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family.  
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 35 57 1 (POTENTIAL).  
 FT DOMAIN 58 64 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 65 85 2 (POTENTIAL).  
 FT DOMAIN 101 122 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 101 122 3 (POTENTIAL).  
 FT DOMAIN 123 144 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 145 166 4 (POTENTIAL).  
 FT DOMAIN 167 184 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 185 208 5 (POTENTIAL).  
 FT DOMAIN 209 265 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 266 290 6 (POTENTIAL).  
 FT DOMAIN 291 295 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 296 320 7 (POTENTIAL).  
 FT DOMAIN 321 440 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 99 180 BY SIMILARITY.  
 FT CONFLICT 247 247 V -> M (IN REF. 2).  
 SQ SEQUENCE 440 AA; 46954 MW; C888F47650CID2EP CRC64;  
 Query Match 15.1%; Score 349.5; DB 1; Length 440;

Best Local Similarity 30.7%; Pred. No. 3,5e-15;  
 Matches 127; Conservative 59; Mismatches 171; Indels 57; Gaps 18;  
 QY 19 VPQPGSTASGVPEVGLRDVASES-----VALFMLLLDLTRAVAGNAAMVIAKTPALR 74  
 DB 2 VPE-GPG-TANSTPAMGAPSPAGSGVMAALCVIALTR-AANSILALICQPALR 58  
 QY 75 KF--VEVFHCLVDLALTLMTPLAMLSSSALFDHALGGEVACRIYELSCFVSALIS 132  
 DB 59 NTSNFEVLSTFSDMLVGLVMPAML--NALYGRWVLARGCLLMTAFDWCCSASILN 116  
 QY 133 VSAIVERYVYVHPMRVREVTGTLVASVYGVWVKALAMASVVLARVSEW---CAP 189  
 DB 117 LCLISDLRYLLSLPKIKIKMTPLRALALVIGAMSLAALSFLL--LGHEHGHARP 174  
 QY 190 SVPPGCSLWMSHAYCVLFVFAVLYFLPLLLLVYCSMFARVAAMQHGPLPTWM 249  
 DB 175 PVPGCCRLASLP-----FVLVASGLTFEFLPSGAICFTYCRILLAAKQAVQVASTLTGM 229  
 QY 250 -----ETPRQSESLSRSTWYSSGAPOTTHRTFGGKAAYVLLAVGQPLL 298  
 DB 230 ASQASSETLVQVPTPRPGVESADSRRLATKHSKRL-----KASLTJGLIGMFFV 279  
 QY 299 CWLPFEFLVYALSAOPISITGOVESVTWIGYFCFTSNPFYGLNPOIRGELSKQFVC 358  
 DB 280 TWLPFFVANIYQAV-CDGISGFLP-VLTWLGICSTANPIITPLFMDPKRALGR----- 333  
 QY 359 FFKPAPEELRLP-SREGSIEENFLQFLQGTGCPSESVSRPLSPKQEPRAVD 411  
 DB 334 -FLPCP-----KCPFRQASLASPSLRTSHSGRPGLS-LQGVLPPLP--PPSD 379  
 RESULT 4  
 HH2R\_CANFA STANDARD; PRT; 359 AA.  
 ID HH2R\_CANFA  
 AC P17124;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Histamine H2 receptor (H2R) (Gastric receptor I).  
 GN HRH2.  
 OS Canis familiaris (Dog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 ON NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91110543; PubMed=1703298;  
 RA Gantz I., Schaeffer M., Delvalle J., Logsdon C., Campbell V.,  
 RA Uhler M., Yamada T.;  
 RT "Molecular cloning of a gene encoding the histamine H2 receptor.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 88:429-433(1991).  
 RN [2]  
 RP MUTAGENESIS OF HISTAMINE-BINDING RESIDUES.  
 RX MEDLINE=93015991; PubMed=1356984;  
 RA Gantz I., Delvalle J., Wang L.-D., Tashiro T., Munzert G., Guo Y.-J.,  
 RA Konda Y., Yamada T.;  
 RT "Molecular basis for the interaction of histamine with the histamine  
 RT H2 receptor.";  
 RL J. Biol. Chem. 267:20840-20843(1992).  
 CC -1- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC  
 CC ACID SECRETION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G  
 CC PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.  
 CC -1- TISSUE SPECIFICITY: GASTRIC FUNDUS AND, TO A LESSER EXTENT, IN  
 CC BRAIN.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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CC -----
DR EMBL; M32701; AAA85637.1; -.
DR PIR; A39008; A39008.
DR HSSP; P29274; 1MH.
DR GCRdb; GCR.0014; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF0001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECPEP_F1.1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECPEP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).
FT TRANSDOM 23 44 1 (POTENTIAL).
FT DOMAIN 45 57 CYTOPLASMIC (POTENTIAL).
FT TRANSDOM 58 81 2 (POTENTIAL).
FT DOMAIN 82 92 EXTRACELLULAR (POTENTIAL).
FT TRANSDOM 93 114 3 (POTENTIAL).
FT DOMAIN 115 134 CYTOPLASMIC (POTENTIAL).
FT TRANSDOM 135 159 4 (POTENTIAL).
FT DOMAIN 160 180 EXTRACELLULAR (POTENTIAL).
FT TRANSDOM 181 204 5 (POTENTIAL).
FT DOMAIN 205 234 CYTOPLASMIC (POTENTIAL).
FT TRANSDOM 235 258 6 (POTENTIAL).
FT DOMAIN 259 267 EXTRACELLULAR (POTENTIAL).
FT TRANSDOM 268 289 7 (POTENTIAL).
FT DOMAIN 290 359 CYTOPLASMIC (POTENTIAL).
FT SITE 98 98 ESSENTIAL FOR HISTAMINE BINDING.
FT SITE 186 186 ESSENTIAL FOR TIOTIDINE BINDING AND
FT SITE 186 186 H2 SELECTIVITY.
FT SITE 190 190 IMPLICATED IN HISTAMINE BINDING.
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 91 174 BY SIMILARITY.
FT MUTAGEN 98 98 D->N: ABOLISHES HISTAMINE BINDING.
FT MUTAGEN 186 186 D->A,N: ABOLISHES TIOTIDINE, BUT NOT
FT MUTAGEN 190 190 CIMEIDINE BINDING.
FT MUTAGEN 190 190 T->A,C: DIMINISHED HISTAMINE-STIMULATED
FT ACTIVITY.
SQ SEQUENCE 359 AA; 40201 MM; 37F36412DF5BE805 CRC64;
Query Match 15.1%; Score 349; DB 1; Length 359;
Best Local Similarity 28.7%; Pred. No. 3.2e-15;
Matches 100; Conservative 56; Mismatches 140; Indels 52; Gaps 10;
QY 43 SVAFEFMLLDLTAVAGNAAMVAIVAKTPALKRFV--FVFHICLDVLLAALTMLPMLMS 100
D 22 SVYLVLLVLI---TAGVNVVYGLANGLRRLRLSLNCFIVSLAITDILLGLLVLF--- 74
QY 101 SSALFDHAL---FGEVACRLYLEFSVCFSVSLAIVSAINVERYYVVVHPMYEVRMTLG 157
D 75 -SAFQOLSCRSMSFGKVFVNITYSLDVMICTASLNLFMISLIDRYCAVDPLRYPLITPV 133
QY 158 LVASLVGVWVWVKALMASVIV-IGRVSMEEGR--SVPGCSLQMSHSAVQOLFVVFVAV 214
D 134 RYAVSLVILAWVISTILSLFSLHGNNSRNETSSFNHTTTPKCVQVN-----LVYGLVDGL 188
QY 215 LVFLPLDLLLVVYCSMFVRVARVAAVMOHQPLPTVMETPRORSESLSRSTWYSSGAPOT 274
D 189 VTFYFLPLVLMCTTYRIKRIARDQAKRRIHNSKMAA----- 225
QY 275 TPHTFGGGAQAVVLLVAVGGQFLCWLPRYFSFHLVYVLSAOPISIGQVESVVTWIGYCFE 334
D 226 ---TIGEHKAVTVTLAAVGAFFIICMFYFVYVYRGLKGDAIDNEAFVAVVLMVLYGANS 281
QY 335 TSNPFYGCINRQIQTIGELSKQVCFEKKRPF--DELRLPSRSGSILEEN 380
D 282 ALNPILVATLVNDFRTAYQQLFRC--RPASHNAOETSLRSNSQSOLARN 327

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	P97292;	(Rel.	36,	Created)
Dt	15-JUL-1998	(Rel.	36,	Last sequence update)
Df	15-JUL-1998	(Rel.	36,	Last annotation update)
Dl	16-OCT-2001	(Rel.	40,	Last annotation update)
De	Histamine H2 receptor (H2R) (Gastric receptor I).			
Cn	HRH2.			
Os	Mus musculus (Mouse).			
Oc	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Ox	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
Rn	NCBI_TaxID:10090;			
Rp	[1]			
Rc	SEQUENCE FROM N.A.			
Rd	STRAIN=129/Ola:			
Rm	MEDLINE=97092891; PubMed=8938453;			
Rv	Kobayashi T., Inoue I., Jenkins N.A., Gilbert D.J., Copeland N.G.,			
Rw	"Cloning, RNA expression, and chromosomal location of a mouse			
Ry	histamine H2 receptor gene."			
Rz	Gnomics 37:390-394(1996);			
Sr	- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC ACID SECRETION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.			
Tg	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
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Xr	EMBL; D50096; BAA08792.1; "			
Xs	GCDB; GCR_1155; "			
Xt	MGI:108482; Hrh2.			
Xv	InterPro: IPRO00076; GPCR_Rhodpsn.			
Xw	Pfam: PF00001; 7tm1; 1.			
Xx	PRINTS; PR00237; GPCRRHODPSN.			
Xy	PROSITE; PS00237; G_PROTEIN_REC_P1.1; 1.			
Zk	PROSITE; PS0262; G_PROTEIN_REC_P1.2; 1.			
Zl	G-protein coupled receptor; Transmembrane; Glycoprotein.			
Zm	DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).			
Zn	TRANSMEM 23 44 CYTOPLASMIC (POTENTIAL).			
Zo	DOMAIN 45 57 2 (POTENTIAL).			
Zp	TRANSMEM 58 81 EXTRACELLULAR (POTENTIAL).			
Zq	DOMAIN 82 92 3 (POTENTIAL).			
Zr	TRANSMEM 93 114 CYTOPLASMIC (POTENTIAL).			
Zs	DOMAIN 115 134 EXTRACELLULAR (POTENTIAL).			
Zt	TRANSMEM 135 159 4 (POTENTIAL).			
Zu	DOMAIN 160 179 EXTRACELLULAR (POTENTIAL).			
Zv	TRANSMEM 180 203 5 (POTENTIAL).			
Zw	DOMAIN 204 233 CYTOPLASMIC (POTENTIAL).			
Zx	TRANSMEM 234 257 6 (POTENTIAL).			
Zy	DOMAIN 258 266 EXTRACELLULAR (POTENTIAL).			
Zz	TRANSMEM 267 288 7 (POTENTIAL).			
Aa	DOMAIN 289 358 CYTOPLASMIC (POTENTIAL).			
Bb	SITE 98 ESSENTIAL FOR HISTAMINE BINDING (BY SIMILARITY).			
Bc	SITE 185 ESSENTIAL FOR TIOTIDINE BINDING AND IMPLICATED IN HISTAMINE BINDING (BY SIMILARITY).			
Bd	SITE 189 IMPlicated IN HISTAMINE BINDING (BY SIMILARITY).			
Be	CANBOHD 4 N-LINKED GLCNAC... (POTENTIAL).			
Bf	DISUFLD 91 173 BY SIMILARITY.			
Bg	SEQUENCE 358 AA; 40379 MW; DSDBAIDFIB60927 CRC64;			
Bh	Query Match 14.9%; Score 345; DB 1; Length 358;			
Bi	Best Local Similarity 27.6%;			
Bj	Pred. No. 5,6e-15;			
Bk	Matches 108; Conservative 58; Mismatches 152; Indels 74; Gaps 12;			
Bl	42 BSVALEFMILLDTT-----AVAGNAAMVAVIKTPALRKRY--FWFHLCVLVDLAALTLM 94			



Db 13 DSIALKVTISVLTTLTLEITVAGNVVCLAVSLNRLSLNCFIVSLAATDILLGLVM 72  
QY 95 PLAMISSALDHAL---FGEVACRLYLELSCVPSLAISLVSAINVRYYVHPMRE 151  
Db 73 PF---SAIQSLSEKMFEGGVFCNIYITSLDMLCTASILNLFMISLDRYCAVDDPLKXP 127  
QY 152 VRMTLGLVASVYGVWVWALMASVPLGRVSWEE-----GAPSVPGCSLQMSHAYC 205  
Db 128 VLVPVRAISLFIWVISTLSLST---HLGMSRNKTRGNDTFK--CKVQVN----- 178  
QY 206 QLEFVVAVLFLPLLLILVYCSMPFARVAAQHPLEPTWMEPRORSESLSRSTM 265  
Db 179 EYGVLDGMVTFYLPILIMCTVYRIKFIAREQAKRINHISMKAA----- 224  
QY 266 VTSSGAQPTTHRTFFGGKAAVVLAVGQFLCMLPFSEHLYVALSAQPISTGOVESV 325  
Db 225 -----TIREKRAVTTLAAVWGAFCVCFYFTAFVYRGRLGDDPVNEVVEGI 271  
QY 326 VTWIGYFCFTSNPFYGCILNRIQELSGKOFVCFEKP--AADEELRL-----PSREG 375  
Db 272 VLMIGYANSALNPILYATLNDPRAVYQQLFCHKLASHNSKRTSLRLNLSLSQSRKG 331  
QY 376 SIENFLOLOGTCGCPSESVSRPLSPKQEP 407  
Db 332 RMOEKKPLKIQ-----VMSGTELTHPQSGP 356

RESULT 6  
ALAD\_RABIT STANDARD; PRT; 576 AA.  
ID ALAD\_RABIT STANDARD; PRT; 576 AA.  
AC 002666;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE ALPHA-1D adrenergic receptor (Alpha 1D-adrenoceptor).  
GN ADRA1D.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN 111  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=97182161; PubMed=9030207;  
RA Suzuki F., Miyamoto S., Takita M., Oshita M., Watanabe Y.,  
RA Kakizuka A., Narumiya S., Taniguchi T., Muramatsu I.;  
RT "Cloning, functional expression and tissue distribution of rabbit  
RT alpha 1d-adrenoceptor";  
RL Biochim. Biophys. Acta 1333:6-11(1997).  
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS EFFECT  
CC THROUGH THE INFUX OF EXTRACELLULAR CALCIUM.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC  
DR EMBL: U64032; AAB53098.1; -;  
DR GCRDB: GCR\_1291; -;  
DR InterPro: IPR000276; GPCR\_Rhodopsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCR\_Rhodopsn.  
DR PROSITE: PS00237; G-PROTEIN\_RECEP\_FL\_1; 1.  
DR PROSITE: PS50262; G-PROTEIN\_RECEP\_FL\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.  
FT DOMAIN 1 101  
FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 102 126  
FT DOMAIN 127 138  
FT TRANSMEM 139 164  
FT DOMAIN 165 174  
FT TRANSMEM 175 197  
FT DOMAIN 198 218  
FT TRANSMEM 219 243  
FT DOMAIN 244 256  
FT TRANSMEM 257 280  
FT DOMAIN 281 353  
FT TRANSMEM 354 378  
FT DOMAIN 379 385  
FT TRANSMEM 386 410  
FT DOMAIN 411 576  
FT CARBOHYD 70 70  
FT CARBOHYD 87 87  
FT LIPID 424 424  
FT LIPID 54 59  
FT DOMAIN 78 84  
FT DOMAIN 427 433  
SO SEQUENCE 576 AA; 60266 MW; 21EDF1025D0144CE CRC64;

Query Match 14.9%; Score 345; DB 1; Length 576;  
Best Local Similarity 25.0%; Pred. No. 8.6e-15;  
Matches 128; Conservative 85; Mismatches 198; Indels 102; Gaps 19;

QY 4 SPIPOSSG--NSSTLGRVPOTPGPSTAGVPEVGLRDVASVVAL-FPMLLDLITAVAGN 60  
Db 60 SVVGAGSGEDNRSSAGBEGGAGGGEVNTAAVGLVAGVSAQSVGVFLAFTITAVAGN 119  
QY 61 AAVMAVIAKTPALRKFFV--FVHILCLVDLAALTPLMPLAMSSALFPHALGEVACRLY 118  
Db 120 LVLILSVACNHNLOTVTYTFVNLAVADLLSAIVLPSS--ATMEVGLFMAFGARFCDW 177  
QY 119 LFLSCVPSLAISLVSAINVERYYVHPARYEVRMTLGLVASVLYGVWVWALMASVPLV 178  
Db 178 AAVDVLCTTASILSLCTISVDVRYGVHSLKYPAIMTERKAAATLALLMAVALVSMGPL 237  
QY 179 LGRVSWERGAASVPPGCSLQMSHAYCOL-----FVVVFAVLYPLLLILVYCSMFR 233  
Db 238 LG---WKE---PVPF-----DERFCGITEVGAVFSSLSCLFPLMAVIVWVCRYV 284  
QY 234 VAR--VVAHQGPLPTWMEPRORSES-----LSSRSTWVTSAGAPOT--TPHRTFCGG 283  
Db 285 VARSTTNSLEAG-----VKREKASEVYLRIHCKRAAGAGACAPETRGAKGHTFRSS 337  
QY 284 -----KAAVVLAVGQFLCMLPFSEHLYVALSAQPISTGOVESVVTWIGY 331  
Db 338 LSVRLKFSREKKAKAKTLAIYGVFVLCWPFPPFLPLGSLFPLQPKSEGVFKVIEMLGY 397  
QY 332 FCFPSNPFYGCILNRIQELSGKOFVCFEKP-----PAPEEEL 368  
Db 398 FNSCVNPLPIYCCSSEEFKRAFLRLRCQRRRRRRRPLRVYGHMWRASAGGHPDCL 457  
QY 369 -----RLPREGSIEENLFQLOGTCGCPSESVSRP-----LSPKQEPAAV--DFRIPQI 418  
Db 458 SAGALPGLA-----LALTAAPAPSSAAAPDEGAAAGAKRKKPCARFRMRLGPL 507  
QY 419 AETSEPLEQDLTSDIIMSLSYLRPAASPRLES 451  
Db 508 RRPIT-----QLRAKVSLSLHKIRAGAGQRAEA 535

RESULT 7  
5H6\_MOUSE STANDARD; PRT; 440 AA.  
ID 5H6\_MOUSE STANDARD; PRT; 440 AA.  
AC O9R1C8;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 5-hydroxytryptamine 6 receptor (5-HT-6) (Seroctonin receptor).  
GN HTR6.  
OS Mus musculus (Mouse).

CC Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ; TISSUE=Brain;  
 RA Kohen R., Guthe C.R., Heidman D.E.A., Hamblin M.W.;  
 RL "Mutagenesis studies of the mouse 5-HT6 serotonin receptor.";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-  
 HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION AS  
 A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF THIS  
 RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE  
 CYCLASE. IT HAS A HIGH AFFINITY FOR TRICYCLIC PSYCHOTROPIC DRUGS  
 (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF134158; AAD46490.1; -  
 DR MCD: MGI:1196627; Hcr6.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHOOPS.  
 DR PROSITE: PS00237; G-PROTEIN\_RECPT\_F1\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECPT\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 FT Multigene family.  
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 35 57 1 (POTENTIAL).  
 FT DOMAIN 58 64 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 65 85 2 (POTENTIAL).  
 FT DOMAIN 86 100 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 101 122 3 (POTENTIAL).  
 FT DOMAIN 123 144 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 145 166 4 (POTENTIAL).  
 FT DOMAIN 167 184 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 185 208 5 (POTENTIAL).  
 FT DOMAIN 209 267 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 268 292 6 (POTENTIAL).  
 FT DOMAIN 293 297 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 298 322 7 (POTENTIAL).  
 FT DOMAIN 323 440 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 99 180 BY SIMILARITY.  
 FT CARBOHYD 9 9 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SO SEQUENCE 440 AA; 46998 MW; 4440CDEBE01FEFC C664;  
 Query Match 14.88; Score 344; DB 1; Length 440;  
 Best Local Similarity 28.88; Pred. NO. 7.8e-15;  
 Matches 134; Conservative 59; Mismatches 187; Indels 86; Gaps 19;  
 DB 2 ESSPSSGSSSTLGRVPTGPSTAGVPEVGLDVAASSVAFLLFVLLATVAVAGNA 61  
 1  
 4 EPGPV-----NSST---PACGCPPPAPG-----GSCVNAALCVIYLA-ANNS 45  
 62 AVMAVIAKPAALRKF--VFVFLCLVLDLALTLPLMLSSALFDHALGEVACRLYL 119  
 46 LLIALICHPALRNSTNLFVLSFTSDLMVGLVMPAML--MLYGRWVLAIGCLLMT 103  
 120 FLSCVFLAIVSAIVERYVYVHPARVEMRTGLCVLAVGVVAKLAMASVPL 179  
 104 AFDWMCASSTILNCLISLDRLITLSPRYKRLMTAPRALALILGAWSLAALSFLL 163  
 180 GRVSMEE--GAPSVPPCCSLQMSHSAICQLFVVFVAVFLVLLPLLLLVYCSFRAR 236  
 164 --LGWHELKARTSAPGCCRLLASLP-----YVLVAVSGVTFELPGAGICFTYCRILLAR 216

QY 237 VAAQHGPLPYMWTPRORSESL-----SRSTWVTSSGAPOTPHRTFGCGKAAVLLAV 292  
 1  
 DB 217 KQAVQVAVSLTTGTATAGALETLQVPRPRPGMSADSRLLTKH-----SKKALKASITL 272  
 QY 293 G---GQFLCMLPYFSEFLYVALSAQ-----ISTGQVSVTWITGICFTSNPFYGLN 345  
 1  
 DB 273 GILSMFPVTVLPFF-----VASIAQAVCDICISPLD-VLTWLGVCNSTNPIIYPLFM 326  
 QY 346 RQIGELSKQVCFEKPAREE-----LRLP-----SREG 375  
 1  
 DB 327 RQFRALGRFPVCHCP--PEHRASAPASPMWTSHSGARPGSLQQLVPLPLPNSDSOA 385  
 376 SIENFLQFLQTCGCPSESWSRPLSPKOPPAVDPRIPQIAEE 421  
 386 SGGTSGQLTQQLLPGEA--TRDPPPTAPVYVNFVTSVEPE 429  
 DB 386 SGGTSGQLTQQLLPGEA--TRDPPPTAPVYVNFVTSVEPE 429  
 RESULT 8  
 HH2R\_CAVPO STANDARD; PRT; 359 AA.  
 ID HH2R\_CAVPO  
 AC P47747;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Histamine H2 receptor (H2R) (Gastric receptor 1).  
 GN HRH2.  
 OS Cavia porcellus (Guinea pig).  
 CC Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.  
 CC NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HARTLEY; TISSUE=Liver;  
 RA Traifort E.;  
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC  
 ACID SECRETION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G  
 PROTEINS WHICH ACTIVATE ADENYL CYCLASE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U25440; AAA65713.1; -  
 DR GCRdb: GCR 1168; -  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHOOPS.  
 DR PROSITE: PS00237; G-PROTEIN\_RECPT\_F1\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECPT\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 23 44 1 (POTENTIAL).  
 FT DOMAIN 45 57 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 58 81 2 (POTENTIAL).  
 FT DOMAIN 82 92 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 93 114 3 (POTENTIAL).  
 FT DOMAIN 115 134 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 135 159 4 (POTENTIAL).  
 FT DOMAIN 160 180 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 181 204 5 (POTENTIAL).  
 FT DOMAIN 205 234 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 235 258 6 (POTENTIAL).  
 FT DOMAIN 259 267 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 268 289 7 (POTENTIAL).  
 FT DOMAIN 290 359 CYTOPLASMIC (POTENTIAL).

FT SITE 98 98 ESSENTIAL FOR HISTAMINE BINDING (BY  
 FT SITE 186 186 SIMILARITY).  
 FT SITE 186 186 ESSENTIAL FOR TIOTIDINE BINDING AND  
 FT SITE 190 190 IMPLICATED IN HISTAMINE BINDING (BY  
 FT SITE 190 190 IMPLICATED IN HISTAMINE BINDING (BY  
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 91 174 BY SIMILARITY.  
 SQ SEQUENCE 359 AA: 40556 MW: 58DB81BD8FC30E9 CRC64:  
 Query Match 14.8%; Score 343; DB 1; Length 359;  
 Best Local Similarity 27.0%; Pred. No. 7.5e-15;  
 Matches 99; Conservative 57; Mismatches 146; Indels 64; Gaps 11;

QY 49 MLILDLTAAGNNAVNAVIKTPALRKVV--FVHLCVLDDLALTLPLALSSSLFED 106  
 DB 25 LILILVTVAGNNVVCCLAVGLNRRLSLTNCFIVSLAVTDLGLLVLFP-----SAIYQ 79  
 QY 107 HAL---FGEVACRLYLFLSYCFVSLALISVAINVERYYVHPMYREVMRTGLVASVL 163  
 DB 80 LSCWSSSKFCNITYTSLDWLCTASTLNLPMISLDRICAVTDPLRPVLTTPARVAISL 139  
 QY 164 VGWVWKAALAAVYFVLGRVSWEGAPSVPPG-----CSLQWSHSAVCOLFEVYFAVLYFL 218  
 DB 140 VFIWVISTITSLFSLI--HLGWSNRNEMSKNDITVCKQVQV-----EYGLVDGLVTFY 192  
 QY 219 LPLILILVYCSMRVAVNAOHGPLETWMETPRORSESLSSSTVSTSGAQTTPHR 278  
 DB 193 LPLILIMITYFRIFKIRIARINHGSMKAA----- 225  
 QY 279 TFGGKAAYVLLAVGGOFLLCMLPFSPHLVVALSAQPISTGOVEVVTWIGYFCFTSNP 338  
 DB 226 TIRHKATVTLAAWGMGFIICMPFYTFYVYRGLKGDANVEVEDVWLVGANSALNP 285  
 QY 339 FFYGCNLROIRGELSKEQVCFKPAPEELRLP---SREGSIENFILOFGTGPCPSES 395  
 DB 286 ILVYALNRDFTAVYHQLFCC-----RLASHNSHETSLRLNNSQ-LNRSCQCGPRW 334  
 QY 396 -VSRL 400  
 DB 335 QEDKPL 340

RESULT 9  
 HH2R\_HUMAN STANDARD; PRT; 359 AA.  
 AC P25021; Q14464;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DE Histamine H2 receptor (HH2) (Gastric receptor 1).  
 GN HH2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91337087; PubMed=1714721;  
 RA Gantz I., Munzert G., Tashiro T., Schaeffer M., Wang L.-D.,  
 RA DelValle J., Yamada T.;  
 RT "Molecular cloning of the human histamine H2 receptor.";  
 RL Biochem. Biophys. Res. Commun. 178:1386-1392(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Liver;  
 RX MEDLINE=95275318; PubMed=7755641;  
 RA Nishi T., Koike T., Oka T., Maeda M., Futai M.;  
 RT "Identification of the promoter region of the human histamine H2-  
 RT receptor gene.";  
 RL Biochem. Biophys. Res. Commun. 210:616-623(1995).  
 RN [3]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=9297624; PubMed=10371214;  
 RA Murakami H., Sun-Wada G., Matsunoto M., Nishi T., Wada Y., Futai M.;  
 RT "Human histamine H2 receptor gene: multiple transcription initiation  
 RT and tissue-specific expression.";  
 RL FEBS Lett. 451:327-331(1999).  
 RN [4]  
 RP SEQUENCE OF 4-351 FROM N.A., AND POLYMORPHISM.  
 RC TISSUE=Brain;  
 RX MEDLINE=96414531; PubMed=8817552;  
 RA Orange P.R., Heath P.R., Wright S.R., Pearson R.C.A.;  
 RT "Allelic variations of the human histamine H2 receptor gene.";  
 RL Neuroreport 7:1293-1296(1996).  
 RN [5]  
 RP REVIEW.  
 RX MEDLINE=98042107; PubMed=9374694;  
 RA DelValle J., Gantz I.;  
 RT "Novel insights into histamine H2 receptor biology.";  
 RL Am. J. Physiol. 273:G987-G996(1997).  
 CC -I- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC  
 CC ACID SECRETION. ALSO APPEARS TO REGULATE GASTROINTESTINAL MOTILITY  
 CC AND INTESTINAL SECRETION. POSSIBLE ROLE IN REGULATING CELL GROWTH  
 CC AND DIFFERENTIATION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY  
 CC G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE AND, THROUGH A SEPARATE  
 CC G PROTEIN-DEPENDENT MECHANISM, THE PHOSPHOINOSITIDE/PROTEIN KINASE  
 CC (PKC) SIGNALING PATHWAY (BY SIMILARITY).  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -I- MISCELLANEOUS: ANTAGONISTS FOR THIS RECEPTOR HAVE PROVEN TO BE  
 CC EFFECTIVE THERAPY FOR ACID PEPTIC DISORDERS OF THE  
 CC GASTROINTESTINAL TRACT. CERTAIN ANTAGONISTS ARE USED IN THE  
 CC TREATMENT OF NEUROPSYCHIATRIC AND NEUROLOGICAL DISEASES SUCH AS  
 CC SCHIZOPHRENIA, ALZHEIMER'S DISEASE AND PARKINSON'S DISEASE.  
 CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL; M64799; AAA58647.1; -;  
 DR EMBL; D49783; BA08618.1; -;  
 DR EMBL; AB023486; BA084279.1; -;  
 DR EMBL; X96133; CA06832.1; -;  
 DR PIR; JH0449; JH0449.  
 DR GCRDB; GCR\_0176; -;  
 DR GCRDB; GCR\_1836; -;  
 DR GCRDB; GCR\_2080; -;  
 DR MTM; 142703; -;  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEP\_FL\_1; 1.  
 DR PROSITE; PS50262; G-PROTEIN\_RECEP\_FL\_2; 1.  
 KM G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.  
 FT DOMAIN 1 22  
 FT TRANSSEM 23 44  
 FT DOMAIN 45 57  
 FT TRANSSEM 58 81  
 FT DOMAIN 82 92  
 FT TRANSSEM 93 114  
 FT DOMAIN 115 134  
 FT TRANSSEM 135 159  
 FT DOMAIN 160 180  
 FT TRANSSEM 181 204  
 FT DOMAIN 205 234  
 FT TRANSSEM 235 258  
 FT DOMAIN 259 267  
 FT TRANSSEM 268 289  
 FT DOMAIN 290 359  
 FT SITE 98 98  
 ESSENTIAL FOR HISTAMINE BINDING (BY

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FT SITE 186 186 SIMILARITY).
FT SITE 186 186 ESSENTIAL FOR TIOTIDINE BINDING AND
FT SITE 186 186 IMPlicated IN H2 SELECTIVITY (BY
FT SITE 186 186 IMPLICATED IN HISTAMINE BINDING (BY
FT SITE 186 186 SIMILARITY).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 91 174 BY SIMILARITY.
FT VARIANT 217 217 N -> D.
FT VARIANT 231 231 /FTID=VAR_009958.
FT VARIANT 231 231 K -> R.
FT VARIANT 268 268 /FTID=VAR_009959.
FT VARIANT 268 268 V -> M.
FT CONFLICT 133 133 V -> A (IN REF. 4).
FT CONFLICT 175 175 K -> N (IN REF. 4).
FT CONFLICT 207 207 K -> R (IN REF. 4).
SQ SEQUENCE 359 AA; 40098 MW; 9835AE2BA60B980F CRC64;

Query Match 14.7%; Score 340; DB 1; Length 359;
Best Local Similarity 28.0%; Pred. No. 1.1e-14;
Matches 97; Conservative 57; Mismatches 134; Indels 58; Gaps 9;

OY 49 MLLDLTAAGNAVAVIAKTPALRKFV--FVHCLVDLLAALTMPLAMSSALFD 106
DB 25 LAVILITVAGNVVCLAVGLNRRLTNCFIVSLAITDLLGLLPF-----SAIQ 79
OY 107 HAL---FGEVACRLYLFLSVGCVSLATLSAIVNERYVYVHPREYVMTGLVASVL 163
DB 80 LSCWMSGKFCNCTITSLDWLCTASTINLPMISLDRCAMDPRLPVLTVPVRAISL 139
OY 164 VGWVWKLAMASVPV-LGRVSWMEGAPS--VPPCSLQMSHSAVCOLFVAVAYELLFP 220
DB 140 VLIIVISITISFLSIHGMNSRNETSKGNHTTSCKVQVN-----EYGLVDGLVTFLP 194
OY 221 LLLILVYVCSMFARVAAVMOHGPLPTMETPPRORSLSLSRSTWVSSGAPOTTPHRTF 280
DB 195 LLMICITYIRIFKVAROAKRINHSSKAA-----TI 227
OY 281 GCGAAVAVLLAVGGQFLMLPFSPFHLVYVLSAQPISITGOVESVMTWIGVCFSTSPFE 340
DB 228 REKATVTLAAVWGAFTICMFPFTAFYRGLRGDDDAINEVLEIVLMLGTANSALNPIL 287
OY 341 YGCLNROIKELSKQVCFKPAPEELRLPSREG---SIEENFLQ 383
DB 288 YVALNRDPRTGYQLFCC-----RLANRSHKTSLSNSNQ 323

RESULT 10
5H6_RAT STANDARD; PRT; 436 AA.
AC P31388;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 5-hydroxytryptamine 6 receptor (5-HT-6) (serotonin receptor)
DE (ST-817).
GN HTR6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Striatum;
RX MEDLINE=93196608; PubMed=7680751;
RA Monma F.J., Jr., Shen Y., Ward R.P., Hamblin M.W., Sibley D.R.;
RT "Cloning and expression of a novel serotonin receptor with high
RT affinity for tricyclic psychotropic drugs.";
RL Mol. Pharmacol. 43:320-327(1993).
RP SEQUENCE FROM N.A.
RX MEDLINE=93277562; PubMed=8389146;

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RA Rat M., Trailfort E., Arrang J.-M., Tardivel-Lacombe J., Diaz J.,
RA Leurs R., Schwartz J.-C.;
RT "A novel rat serotonin (5-HT6) receptor: molecular cloning,
RT localization and stimulation of cAMP accumulation.";
RL Biochem. Biophys. Res. Commun. 193:268-276(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RA Marital R.;
RL Submitted (xxx-1993) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR
CC 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
CC AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
CC CYCLASE. IT HAS A HIGH AFFINITY FOR TRICYCLIC PSYCHOTROPIC DRUGS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: LOCALIZED EXCLUSIVELY IN THE CENTRAL NERVOUS
CC SYSTEM, PREDOMINANTLY IN THE CORPUS STRIATUM BUT ALSO IN VARIOUS
CC LIMBIC AND CORTICAL REGIONS.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L03202; AAA40618.1; -.
DR EMBL: S62043; AAB26908.1; -.
DR EMBL: L19656; AAA40611.1; -.
DR GCRDB: GCR_0723; -.
DR GCRDB: GCR_0719; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 57 1 (POTENTIAL).
FT DOMAIN 58 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 85 2 (POTENTIAL).
FT DOMAIN 86 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 122 3 (POTENTIAL).
FT DOMAIN 123 144 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 145 166 4 (POTENTIAL).
FT DOMAIN 167 184 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 185 208 5 (POTENTIAL).
FT DOMAIN 209 265 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 266 290 6 (POTENTIAL).
FT DOMAIN 291 295 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 321 436 7 (POTENTIAL).
FT DOMAIN 321 436 CYTOPLASMIC (POTENTIAL).
FT DISULFID 9 9 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 57 180 BY SIMILARITY.
FT CONFLICT 336 436 L -> V (IN REF. 1).
FT CONFLICT 336 436 PCVCHPEHRRALPPPCGLTVAVPDAASCSRCICLCRO
FT CONFLICT 336 436 TQITQPLQAGPACSSOPSCLEPGRHHPGPPWST
FT CONFLICT 336 436 SLISQITLMSLYGRHISVPP -> HASTVPSSTQPLPLVAV
FT CONFLICT 336 436 DLSCRCOTRPOLOVIALPLPNSDSASGSGSLTAAQ
FT CONFLICT 336 436 LLLEGATRDPPPTATVTVNFEVDSVEPEIRPHPLSSP
FT CONFLICT 336 436 VN (IN REF. 1)

SQ SEQUENCE 436 AA; 46922 MW; 6BC00F6A3CBA5FB4 CRC64;

Query Match 14.6%; Score 338.5; DB 1; Length 436;
Best Local Similarity 28.4%; Pred. No. 1.7e-14;
Matches 129; Conservative 58; Mismatches 171; Indels 97; Gaps 20;

OY 2 ESSPIPOSGNSSTLGRVPTPGSTASGVPEVGLRDVASEVALFMLLDLTAVAGNA 61

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Db 4 EPCGV-----NSST---PAMGPPPPAPG-----GSGWVAALCVIIVLTA-AANS 45
QY 62 AVMAVIKTPALRKF--VFVPHLCVLDLALTLMPALMLSSSALFPHALGCVACRYL 119
Db 46 LLVILCTOPALRNTSNFVLSTSDMLVGLVMPML--NALYGRWVLARGLCLMT 103
QY 120 FLVCFVSLATLSAIVNRYVYVHPMYREVTGLGVSVLVGVVVKALMASVPL 179
Db 104 AFDVMCSASATLNCILSDRYLLILSLPKRLKMTAPRALALLGAMSLAALSLPL 163
QY 180 GRVSWEE-GAPSV-PGCSLOWSHSAYCOL-----FVVFAVLYELLPLLLIIVYCSMF 232
Db 164 --LGMHELGKARTAPG-----QCRILASLPFVLASGVMEFLPSGALICTYCHIL 212
QY 233 RVAVAMOHGRLPTWM-----ETPRSESSSSSTWVTSSGAPQTPHRTFG 281
Db 213 LAARKQAVQVASTLTGTAGALETLQVPRTPRPMESADSRLATKHSRKAL----- 264
QY 282 GKAAVVLAVGQFLCLMLPFYFSLHYVALSAPISTQVSVYTWIGFCTSNPFY 341
Db 265 --KASLTGLILGMFETWLPFVANAQAV-CDCISGLFD-VLTWLGYNSTMNPLTY 320
QY 342 GCLNRQIRGELSKQVCFKPAPEELRLP-----SREGSI 377
Db 321 PLFMRDEKRALGRPLPCVHCP-PENRPLALPPPCGPIITAVPDQASACSRCLICRQTOI 379
QY 378 EENLOFLQCT--GC-----PSESWSRPLSPKQEP 407
Db 380 QTP---LQGAPRACSSQSPFCLELRPPGTPRHP 410

RESULT 11
B3AR_RAT
ID B3AR_RAT STANDARD: PRT: 400 AA.
AC P26255;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Beta-3 adrenergic receptor.
GN ADRB3 OR ADRB3R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92084710; PubMed=1721063;
RA Muzain P., Revelli J.-P., Kuhne F., Gocayne J.D., McCombie W.R.,
RA Venter J.C., Giacobino J.-P., Fraser C.M.;
RT "An adipose tissue-specific beta-adrenergic receptor. Molecular
RT cloning and down-regulation in obesity."
RL J. Biol. Chem. 266:24053-24058(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93178631; PubMed=8382630;
RA Bensaid M., Kachhad M., Rodriguez M., Je Fur G., Caput D.;
RT "The rat beta 3 adrenergic receptor gene contains an intron."
RL FEBS Lett. 318:223-226(1993).
CC - FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AND
CC THERMOGENESIS.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - TISSUE SPECIFICITY: WHITE AND BROWN ADIPOSE TISSUES, AND DIGESTIVE
CC TRACT.
CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M74716; AAA74470.1; -
DR EMBL: S73473; AAB20702.1; -
DR EMBL: S56481; AAB25520.1; -
DR EMBL: S56152; AAB25521.1; -
DR PIR: A41679; A41679
DR PIR: S29808; S29808.
DR PIR: A53281; A53281.
DR HSPB: P07700; IDEP.
DR GCRDB: GCR_0287; -
DR GCRDB: GCR_0622; -
DR GCRDB: GCR_0732; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHDOPSN.
DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 36
FT TRANSSEM 37 60
FT DOMAIN 61 69
FT TRANSSEM 70 88
FT DOMAIN 89 108
FT TRANSSEM 109 130
FT DOMAIN 131 152
FT TRANSSEM 153 175
FT DOMAIN 176 200
FT TRANSSEM 201 222
FT DOMAIN 223 289
FT TRANSSEM 290 311
FT DOMAIN 312 323
FT TRANSSEM 324 344
FT DOMAIN 345 400
FT CARBOHYD 8 8
FT DISULFID 26 26
FT LIPID 107 186
FT CONFLICT 358 358
FT CONFLICT 234 235
SQ SEQUENCE 400 AA; 43146 MW; D588540C4B2CE813 CRC64;

Query Match 14.58; Score 337; DB 1; Length 400;
Best Local Similarity 28.28; Pred. NO. 2e-14;
Matches 120; Conservative 65; Mismatches 188; Indels 52; Gaps 17;

QY 4 SPIPOSSGNSSTLGRVPO-TPGPSTAGVPEVGRDVASEVALFMILLDTLTVAGNAA 62
Db 2 APWHKNSLAFWSDAPTLDPSSAANTGLPGV-----PAAALAGALLALATVGGILL 54
QY 63 VMAVIKTPALRKF--VFVPHLCVLDLALTLMPALMLSSSALFPHALGCVACRYL 120
Db 55 VITAIARTPLQITITVNFVSLATADLVGLVMPG--ATLALTGHMPLGATGCELTMS 112
QY 121 LSCVFSALTSAINVRYVYVHPMYREVTGLGVSVLVGVVVKALMASVPL 180
Db 113 VDLVLCVTAIETLCAADRYLATNPLRGTLYTKRRARAVALVWIVSATVSPFAPLMS 172
QY 181 RVSWEGAPSVPPGCSLOWSHSAYCOL-----FVVFAVLYELLPLLLIIVYCSMPRVA 235
Db 173 Q-WWRVGADEAAGCH---SNPRCCSPASNNPYALLSSSVFYPLVLMFLVYARVFAVA 228
QY 236 ---RVAAMOHGRLPTWMETPR--ORSESLSSSTWVTSSGAP--TPPHR--TFGGGKA 285
Db 229 KRORRLRLRELGRPP--EESPRSPSRSPSPATVGTPTASDGVPCGRPARLPLGCHRA 287

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RESULT 13  
ALAD\_RAT  
ID ALAD\_RAT STANDARD: PRT: 561 AA.  
AC P23944;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Alpha-ID adrenergic receptor (Alpha ID-adrenoceptor) (Alpha-1A adrenergic receptor) (RA42).  
GN ADRA1D OR ADRA1A.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
[1]  
NP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain cortex;  
RX MEDLINE=91177889; PubMed=1706716;  
RA Lomasney J.W., Cotecchia S., Lorenz W., Leung W.-Y., Schwinn D.A., Yang-Feng T.L., Brownstein M., Lefkowitz R.J., Caron M.G.;  
RT "Molecular cloning and expression of the cDNA for the alpha 1A-adrenergic receptor. The gene for which is located on human chromosome 5.";  
RT J. Biol. Chem. 266:6365-6369(1991).  
[2]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=95114877; PubMed=7815325;  
RA Schwin D.A., Johnston G.I., Page S.O., Mosley M.J., Wilson K.H., Norman N.P., Campbell S., Fidock M.D., Furness L.M., Parry-Smith D.J., Peter B., Bailey D.S.;  
RT "Cloning and pharmacological characterization of human alpha-1 adrenergic receptors: sequence corrections and direct comparison with other species homologues.";  
RT J. Pharmacol. Exp. Ther. 272:134-142(1995).  
RL J. FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS EFFECT THROUGH THE INFLOW OF EXTRACELLULAR CALCIUM.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: VAS DEFERENS, HIPPOCAMPUS, CEREBRAL CORTEX, AORTA, BRAIN STEM, HEART AND SPLEEN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC -----  
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CC -----  
CC EMBL: M60654; AAA63477.1; -;  
CC EMBL: L31771; AAB59704.1; -;  
CC PIR: A38731; A38731.  
DR GCRDB; GCR\_0123; -;  
DR GCRDB; GCR\_1534; -;  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; G-PROTEIN\_RECEP\_FL\_1; 1.  
DR PROSITE: PS00237; G-PROTEIN\_RECEP\_FL\_2; 1.  
DR PROSITE: PS50262; G-PROTEIN\_RECEP\_FL\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Palmitate.  
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.  
FT DOMAIN 1 90  
FT TRANSMEM 91 115  
FT DOMAIN 116 127  
FT TRANSMEM 116 127  
FT TRANSMEM 128 153  
FT DOMAIN 154 163  
FT TRANSMEM 164 186  
FT DOMAIN 187 207  
FT TRANSMEM 208 232  
FT DOMAIN 233 245  
FT TRANSMEM 246 269  
FT DOMAIN 270 342  
FT TRANSMEM 343 367

FT DOMAIN 368 374  
FT TRANSMEM 375 399  
FT DOMAIN 400 561  
FT CARBOHYD 60 60  
FT CARBOHYD 76 76  
FT LIPID 413 413  
FT DOMAIN 21 57  
FT DOMAIN 416 421  
FT CONFLICT 424 483  
SQ SEQUENCE 561 AA: 59354 MW: B6537DCADAF7BE27 CRC64:  
Query Match 14.5%; Score 335.5; DB 1; Length 561;  
Best Local Similarity 25.7%; Pred. No. 3,3e-14;  
Matches 125; Conservative 81; Mismatches 195; Indels 85; Gaps 19;  
QY 6 IPOSSGNSSTLGR-----VPQPGSPASGVPEGLDVASEVAL-FFMILLD 53  
Db 42 VPQATGGAVGTGSGEDNOSTGEBGAASGVNSAAGLVAGVGAVFLAFL 101  
QY 54 LRAVAGNAVMAYIAKTPALRKFV--FVHLCLVDLLALTTMLPLAMSSALFDHALFG 111  
Db 102 LRAVAGNLVLIVLSVACNRHLQFTVNYFIYLAVALDLLSAVLPS--ATMEVLGFMAFG 159  
QY 112 EVACRIYFLSVCFVSLATLSVAIVERIYVHMRKREVRTLGLVAVGVVAKL 171  
Db 160 RFECDDVAWADVLCCTASTLCTISVDYVGRSHLKYPAINTERKAAIALLAVAL 219  
QY 172 AMASVPLGRVSWEEGAPSVPCGSLQWSHSAQCQ-----FVAVVAYFLPLLLIV 226  
Db 220 VVSVPGLG---WKE---FYPP-----DERCGITEEGVAFESVCSFYLPMAVIY 266  
QY 227 VYCSMRVAR--VAAMQHPPLTMMETPRQSE---SLSRSTMTVSSGAP--QTPPHRT 279  
Db 267 MYCRVYVARSTRLSEAG---IKREPGKASEVLRHRCGAATSAKVGPGTOSKGT 322  
QY 280 FGCG-----KAANVLLAVGQPLCLPFPFHLIYALASQPISTQGVSVY 327  
Db 323 LRSLSVRLKTSREKRAKTAIVGVFLCFEPFVLPGLSLPPLKPSGCVKYIE 382  
QY 328 WIGYFCFTSNPFYGCILNRIGELSKQVCFKPAPEEELRLRSRGSTEENFLQFLOG 387  
Db 383 WIGYFSCVNPILPPSSNE-----FKRAFLRLRQCR---RRRLAAVVG 427  
QY 388 TGCPSSEWVRP--LPSPKQEPVADFRI--PGQIAETSEFLQQLSDIIMSQYLR 442  
Db 428 HHWRASGTGARSDCAPSPRIAPGAPLALTAPHGAGSADTPE-----TQDSVSSSR--K 479  
QY 443 PAASPR 448  
Db 480 PASALR 485  
RESULT 14  
BAAR\_MEIGA  
ID BAAR\_MEIGA STANDARD: PRT: 428 AA.  
AC P43141;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Beta-4C adrenergic receptor.  
GN ADRA4C.  
OS Melagris gallopavo (Common turkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.  
OX NCBI\_TaxID=9103;  
[1]  
NP SEQUENCE FROM N.A.  
RC MEDLINE=95014249; PubMed=7929160;  
RA Chen X.-H., Harden T.K., Nicholas R.A.;  
RT "Molecular cloning and characterization of a novel beta-adrenergic



```

RT receptor.
RL J. Biol. Chem. 269:24810-24819(1994).
CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BROAD TISSUE DISTRIBUTION.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; U13977; AAA62150.1; -.
CC EMBL; U13978; AAA62151.1; -.
CC HSSP; P07700; IDEP.
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCR_Rhodopsn.
CC PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
CC PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSMM 26 49 1 (POTENTIAL).
FT DOMAIN 50 58 CYTOPLASMIC (POTENTIAL).
FT TRANSMM 59 77 2 (POTENTIAL).
FT DOMAIN 78 97 EXTRACELLULAR (POTENTIAL).
FT TRANSMM 98 119 3 (POTENTIAL).
FT DOMAIN 120 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMM 142 164 4 (POTENTIAL).
FT DOMAIN 165 189 EXTRACELLULAR (POTENTIAL).
FT TRANSMM 190 211 5 (POTENTIAL).
FT DOMAIN 212 261 CYTOPLASMIC (POTENTIAL).
FT TRANSMM 262 283 6 (POTENTIAL).
FT DOMAIN 284 294 EXTRACELLULAR (POTENTIAL).
FT TRANSMM 295 315 7 (POTENTIAL).
FT DOMAIN 316 428 CYTOPLASMIC (POTENTIAL).
FT CARBOHD 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFD 96 175 BY SIMILARITY.
FT LIPID 329 329 PALMITATE (BY SIMILARITY).
SO SEQUENCE 428 AA; 47398 MW; E82DC920B3B6889 CRC64.

Query Match 14.5%; Score 335; DB 1; Length 428;
Best Local Similarity 27.3%; Pred. NO. 2.8e-14;
Matches 115; Conservative 59; Mismatches 179; Indels 68; Gaps 15;

OY 22 TPGPSTAGSVPYGLRDVASEVALFPHLLD-LRAVAGNAVAVIAKTPALRKF--VF 78
DB 2 TPLPAGNGSVPCSWAAVALSRQMAVGAALSTILVIVAGNLLVIAVIAATPRLQTMVNF 61
OY 79 VPHLCVLDLALTLPLMLAMSSALFDHALGEVACRLYLPLSCFVSLATLSAIVN 138
DB 62 VTSLACADLVKGLLVYPR--ATILLSGHWPGYVCELTSLDVLCTVASTETICATV 119
OY 139 ERYVVVHPMYREVMRTGLVASVLGVVWVAKALAMASVPLGVGWSMEGAPSPGCSIQ 198
DB 120 DRYLAITAPLYEALVTGKRAVAVVCMVAISAFISFLPMNH--MWRDQADQAVRC-- 175
OY 199 WSHSAVQQL-----FVVVFAVLFLPLLLLVYCSMRVA-----RVAAMQHG 243
DB 176 YDDPRCCEVTNMTVAIVSSTVSFVPLVMTFVVVRAVAVTRVQVLGKDKVRLDEN 235
OY 244 PLPMTETPRGSRSLSTWTSAGAPQTPHRTFG--GSKAAVLLAVAGCOFLICWL 301
DB 236 P-----SLSSR-----GGWRRPSRLAIKEKALKLTGICITIGTPTLCWL 275
OY 302 PYFSFHLVVALSAOPISIGQVBSVVTWIGYFCFTSNPFYGLCINQRIQELSKEQVCEPK 361

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DB 276 PEFVANL-IKVCRPLVPDQLEFLFNLWIGVNSANPPIY-CRSPDFPSAFKLLCC--- 330
OY 362 PAPEELRLPSREGSIEENFLQFLQGTGCPSESWSRPLPSKQPPAVDRIPQIDEE 421
DB 331 -----PRADRRLHAAPDQPHCSC-----AFSPGDMEDSKAVD--PGLHRED 373
OY 422 T 422
DB 374 S 374

RESULT 15
ALAD_HUMAN STANDARD: PRT: 572 AA.
ID ALAD_HUMAN
AC P25100.
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-1D adrenergic receptor (Alpha 1D-adrenoceptor) (Alpha-1A
DE adrenergic receptor).
GN ADRA1D OR ADRA1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Hippocampus;
RX MEDLINE=92028892; PubMed=1656955;
RA Bruno J.F., Whitaker J., Song J., Berelowitz M.;
RT "Molecular cloning and sequencing of a cDNA encoding a human alpha 1A
RL adrenergic receptor."
RN Biochem. Biophys. Res. Commun. 179:1485-1490(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Hippocampus;
RX MEDLINE=94239386; PubMed=8183249;
RA Forray C., Bard J.A., Wetzel J.M., Chiu G., Shapiro E., Tang R.,
RA Lepor H., Hartig P.R., Weinschenk R.L., Branchek T.A.,
RA Gluchowski C.;
RT "The alpha 1-adrenergic receptor that mediates smooth muscle
RT contraction in human prostate has the pharmacological properties of
RL the cloned human alpha 1c subtype."
RN Mol. Pharmacol. 45:703-708(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95114877; PubMed=7815325;
RA Schwin D.A., Johnston G.I., Page S.O., Mosley M.J., Wilson K.H.,
RA Wortman N.P., Campbell S., Fiddock M.D., Furness L.M.,
RA Parry-Smith D.J., Peter B., Bailey D.S.;
RT "Cloning and pharmacological characterization of human alpha-1
RT adrenergic receptors: sequence corrections and direct comparison with
RT other species homologues."
RN J. Pharmacol. Exp. Ther. 272:134-142(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=94296402; PubMed=8024574;
RA Weinberg D.H., Trivedi P., Tan C.P., Mitra S., Perkins-Barrow A.,
RA Borowski D., Strader C.D., Bayne M.;
RT "Cloning, expression and characterization of human alpha adrenergic
RT receptors alpha 1a, alpha 1b and alpha 1c."
RN Biochem. Biophys. Res. Commun. 201:1296-1304(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE-Placenta, and Prostate;
RX MEDLINE=95265059; PubMed=7746284;
RA Edenshade T.A., Hirasawa A., Tsujimoto G., Tanaka T., Yano J.,
RA Mineman K.P., Murphy T.J.;
RT "Cloning of the human alpha 1d-adrenergic receptor and inducible
RT expression of three human subtypes in SK-N-MC cells."
RL Mol. Pharmacol. 47:977-985(1995).
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS EFFECT

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[illegible]





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|||||
Db 181 RVSEBAPSVPCSLQWMSHAYCOLFVVFAVLYELLPLLLLVYCSMFRAVAAM 240
OY 241 OHGLPTWMEPRORSLSRSMTVSSGAPOTPHRTGGGKAAYVLLAVGGQFLCW 300
Db 241 OHGLPTWMEPRORSLSRSMTVSSGAPOTPHRTGGGKAAYVLLAVGGQFLCW 300
OY 301 LPVFSFLVYALSAQPISTGVESVWVWIGFCFTSNPFYGCINROI RGLSKQVCF 360
Db 301 LPVFSFLVYALSAQPISTGVESVWVWIGFCFTSNPFYGCINROI RGLSKQVCF 360
OY 361 KPAPEELRLPSREGSIEENFLQGTGCPSESWSRPLPSKQEPVADFRIPQIAE 420
Db 361 KPAPEELRLPSREGSIEENFLQGTGCPSESWSRPLPSKQEPVADFRIPQIAE 420
OY 421 ETSEFLQOULTSDIIMSDSYLRPAASPRLES 451
Db 421 ETSEFLQOULTSDIIMSDSYLRPAASPRLES 451
```

## RESULT 2

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09BZJ8 ID 09BZJ8 PRELIMINARY: PRT: 417 AA.
AC 09BZJ8:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR.
GN GPR61.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105913; PubMed=11165367;
RA Lee D.K., Cheng R., Nguyen T., Liu Y., Brown M., Lynch K.R.,
RA George S.R., O'Dowd B.F.;
RT "Identification of four novel human G protein-coupled receptors
RT expressed in the brain.";
RL Brain Res. Mol. Brain Res. 86:13-22(2001).
DR EMBL: AF317652; AAK12637.1; -
DR Interpro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 417 AA; 45606 MW; 3475BD4F1A714FF2 CRC64;
```

Query Match Best Local Similarity 90.9%; Score 2106; DB 4; Length 417;

Matches 409; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
OY 1 MESSPIPOSSNSTLGRVPTGPSTASGVPEVGLRDVASEVALFFMLLDLTAAAGN 60
Db 1 MESSPIPOSSNSTLGRVPTGPSTASGVPEVGLRDVASEVALFFMLLDLTAAAGN 60
OY 61 AAVAAYIAKTPALKKFFVFLCLVDLLAATLTKPLMLSSALFDHALPGEVACRLYL 120
Db 61 AAVAAYIAKTPALKKFFVFLCLVDLLAATLTKPLMLSSALFDHALPGEVACRLYL 120
OY 121 LSVCFVSLAITSVAINVERYYVHPRYERMTGLVAVLVGVWVKALAMASVPLG 180
Db 121 LSVCFVSLAITSVAINVERYYVHPRYERMTGLVAVLVGVWVKALAMASVPLG 180
OY 181 RVSEBAPSVPCSLQWMSHAYCOLFVVFAVLYELLPLLLLVYCSMFRAVAAM 240
Db 181 RVSEBAPSVPCSLQWMSHAYCOLFVVFAVLYELLPLLLLVYCSMFRAVAAM 240
OY 241 OHGLPTWMEPRORSLSRSMTVSSGAPOTPHRTGGGKAAYVLLAVGGQFLCW 300
Db 241 OHGLPTWMEPRORSLSRSMTVSSGAPOTPHRTGGGKAAYVLLAVGGQFLCW 300
```

```
|||||
OY 301 LPVFSFLVYALSAQPISTGVESVWVWIGFCFTSNPFYGCINROI RGLSKQVCF 360
Db 301 LPVFSFLVYALSAQPISTGVESVWVWIGFCFTSNPFYGCINROI RGLSKQVCF 360
OY 361 KPAPEELRLPSREGSIEENFLQGTGCPSESWSRPLPSKQEPVADFRIPQIAE 420
Db 361 KPAPEELRLPSREGSIEENFLQGTGCPSESWSRPLPSKQEPVADFRIPQIAE 420
```

## RESULT 3

```
09BZJ7 ID 09BZJ7 PRELIMINARY: PRT: 368 AA.
AC 09BZJ7:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR.
GN GPR62.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105913; PubMed=11165367;
RA Lee D.K., Cheng R., Nguyen T., Liu Y., Brown M., Lynch K.R.,
RA George S.R., O'Dowd B.F.;
RT "Identification of four novel human G protein-coupled receptors
RT expressed in the brain.";
RL Brain Res. Mol. Brain Res. 86:13-22(2001).
DR EMBL: AF317653; AAK12638.1; -
DR Interpro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 368 AA; 37628 MW; 9CFF95298D12C75 CRC64;
```

Query Match Best Local Similarity 18.9%; Score 438.5; DB 4; Length 368;

Matches 127; Conservative 55; Mismatches 146; Indels 71; Gaps 14;

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OY 40 ASE---SVAFFMLLDLTAVAGNAAMVIAKTPALKKFFVFLCLVDLLAATLTKPL 96
Db 9 ASEVAGSLGLLAAVAVVAGLNGALLVYLRPRGLRDLALYHLCLVDLLAASIMPL 68
OY 97 AMSSSAL-EDHALPGEVACRLYFLSVCFVSLAITSVAINVERYYVHPRYERMT 155
Db 69 GLLAAPPGLGRVRLGPAFCRAARFLSAALLPACTLGVAMGLARLYVHPRGRPP 128
OY 156 LGIVASLVGVWVKALAMASVPLVGRVSWEBGAPSPGCSLQWMSHAYCOL-----F 208
Db 129 PVL---VLTAVMAAGLGLALSL-----GPPAPPPA-----PARCSVLAGGLGPF 172
OY 209 VVFAVLYELLPLLLLVYCSMFRAVAAMQHPLTWMEPRORSLSRSMTVTS 268
Db 173 RPLWALLAFALPALLLLGAVGIFVVARAALR-PPRPA--RGSRLRSDSLDRLSL- 227
OY 269 SGAPQTPHRTGGGKAAYVLLAVGGQFLCWLPLFSFHLVYALSAQPISTGVESVW 328
Db 228 ---PPLRPR--LPCKAALPALAVGOFACWLPY-----GCACLAARAAAEAAVTV 277
OY 329 IGYFCFTSNPFYGCINROI---GELSKQVCFCKPAPEELRLPSREGSIEENFLQ 385
Db 278 VAASAFAAHPFLGLDRPVKALGLRSLRRL-----GPPVR----- 314
OY 386 QGTGCPSESWSRPLPSKQEPVADFRIPQIAEFTSE 424
Db 315 ---ACTPQAMHPRALLDCLQRPBGPAVGPSEARPDQIRE 350
```

## RESULT 4

090x37  
ID 090x37 PRELIMINARY: PRT: 358 AA.  
AC 090x37  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE HISTAMINE H2 RECEPTOR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N. A.  
RC STRAIN=129SVJ;  
RA Fukushima Y., Asano T., Sugano K.;  
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; AF019138; AAD01634.1; -  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_RHODPSN.  
DR PROSITE; PS00237; G-PROTEIN\_RECPEP\_FL\_1; 1.  
DR PROSITE; PS50262; G-PROTEIN\_RECPEP\_FL\_2; 1.  
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
SQ SEQUENCE 358 AA; 40284 MW; D270C2C66AB7A256 CRC64;

Query Match 15.0%; Score 347; DB 11; Length 358;  
Best Local Similarity 27.6%; Pred. No. 2.5e-22;  
Matches 108; Conservative 58; Mismatches 152; Indels 74; Gaps 12;

QY 42 ESVALFEMLLDLT-----AVAGNAAVAVIAKTPALRKFV--FVHCLVDLLAALTL 94  
DB 13 DSIALKVTISVLTLTITVAAGNVVCLAVSLNRLSLNCFIVSLAATDILLGLLVM 72  
QY 95 PLAMSSALFDHAL---FGEVACHLYFLSYCFVSLAILSYAINVERIYVHPMYE 151  
DB 73 PF-----SAIQLSFKMSFGVFCNITYSLDMVICTASILNFMISLDRYCAVDPLEKYP 127  
QY 152 VRMTGLVASVLVGVWVAKALMASVPVIGRVSWEE-----GAPSVPGCSLONSHSAYC 205  
DB 128 VLVTFRVAISLVFIVWISITLSFLSI--HLGWSNRNGTRGNDTFK--CKQVNA----- 178  
QY 206 QLEVVAVFVFLPLLLILVYVCSMFVARVAAMOHGRLPTWMTTPRQSRSSLSRSTM 265  
DB 179 EYGLGDGMVTFYLPDLIMCTVYRIKFIARQAKRINHISWKAA----- 224  
QY 266 VTSSGAPOTTTHRTFGGKAAVVLAVGQFLLCWLPYFSFHLVYALSAPISTGVESV 325  
DB 225 -----TIREHKAATVTLAAVMGAFIVCMFPYFTAFVYRGLDGDAVNEVVGII 271  
QY 326 VTWIGYFCFTSNPFYGGCLNROINGELSKOFVCFKRP--APEEELRL-----PSREG 375  
DB 272 VLWLGYSANSLNPILYATLNDFRMAVYQDLFCHCKLASHNSHKTSILRLNNSLSRSQSRREG 331  
QY 376 SIENFLOFLOGTGCPSSWSVRPLPSKQEP 407  
DB 332 RMQEEKPLKLO-----VMSGTELTTHPQSGP 356

RESULT 5  
09D282 PRELIMINARY: PRT: 397 AA.  
AC 09D282  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE HISTAMINE RECEPTOR H 2.  
GN HRH2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxId=10090;

RN [1]  
RP SEQUENCE FROM N. A.  
RC STRAIN=C57BL/6J; TISSUE=CECUM;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adech J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barb G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; AK020259; BAB3204.1; -  
DR MGD; MGI:108482; Hrh2.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_RHODPSN.  
DR PROSITE; PS00237; G-PROTEIN\_RECPEP\_FL\_1; 1.  
DR PROSITE; PS50262; G-PROTEIN\_RECPEP\_FL\_2; 1.  
KW G-protein coupled receptor; Glycoprotein; Transmembrane.  
SQ SEQUENCE 397 AA; 44793 MW; BB4719084F4BDD5 CRC64;

Query Match 15.0%; Score 347; DB 11; Length 397;  
Best Local Similarity 27.6%; Pred. No. 2.8e-22;  
Matches 108; Conservative 58; Mismatches 152; Indels 74; Gaps 12;

QY 42 ESVALFEMLLDLT-----AVAGNAAVAVIAKTPALRKFV--FVHCLVDLLAALTL 94  
DB 13 DSIALKVTISVLTLTITVAAGNVVCLAVSLNRLSLNCFIVSLAATDILLGLLVM 72  
QY 95 PLAMSSALFDHAL---FGEVACHLYFLSYCFVSLAILSYAINVERIYVHPMYE 151  
DB 73 PF-----SAIQLSFKMSFGVFCNITYSLDMVICTASILNFMISLDRYCAVDPLEKYP 127  
QY 152 VRMTGLVASVLVGVWVAKALMASVPVIGRVSWEE-----GAPSVPGCSLONSHSAYC 205  
DB 128 VLVTFRVAISLVFIVWISITLSFLSI--HLGWSNRNGTRGNDTFK--CKQVNA----- 178  
QY 206 QLEVVAVFVFLPLLLILVYVCSMFVARVAAMOHGRLPTWMTTPRQSRSSLSRSTM 265  
DB 179 EYGLGDGMVTFYLPDLIMCTVYRIKFIARQAKRINHISWKAA----- 224  
QY 266 VTSSGAPOTTTHRTFGGKAAVVLAVGQFLLCWLPYFSFHLVYALSAPISTGVESV 325  
DB 225 -----TIREHKAATVTLAAVMGAFIVCMFPYFTAFVYRGLDGDAVNEVVGII 271  
QY 326 VTWIGYFCFTSNPFYGGCLNROINGELSKOFVCFKRP--APEEELRL-----PSREG 375  
DB 272 VLWLGYSANSLNPILYATLNDFRMAVYQDLFCHCKLASHNSHKTSILRLNNSLSRSQSRREG 331  
QY 376 SIENFLOFLOGTGCPSSWSVRPLPSKQEP 407  
DB 332 RMQEEKPLKLO-----VMSGTELTTHPQSGP 356

RESULT 6  
09TTM9 PRELIMINARY: PRT: 571 AA.  
AC 09TTM9

DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE ALPHA-1D ADRENERGIC RECEPTOR.  
GN ALPHA-1D.  
OS Sus scrofa (Pig) .  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
OX NCBI\_TaxID=9623;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Uhlen S., Wralth A.;  
RT "Characterization of the pig alpha-1d adrenergic receptor."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC EMBL: AJ250492; CAB59347.1; -  
DR EMBL: AJ250493; CAB59347.1; JOINED.  
DR InterPro: IPR000276; GPCR\_Rhodopsn.  
DR Pfam: PF00001; 7tm1\_1.  
DR PRINTS: PR00237; GPCR\_RHODOPSN.  
DR PROSITE: PS00237; G-PROTEIN\_RECP\_F1\_1; 1.  
DR PROSITE: PS50262; G-PROTEIN\_RECP\_F1\_2; 1.  
KW G-protein coupled receptor; Glycophorin; Receptor; Transmembrane.  
SEQUENCE 571 AA; 60598 MW; BACFPB5C50372B1 CMC64;

Query Match	14.48	Score 333.5	DB 6	Length 571
Best Local Similarity	24.08	Pred. No. 6.3e-21		
Matches 125	Conservative 85	Mismatches 201	Indels 109	Gaps 17

OY	6	IPSSGNSSTLCGRVQ-----TPGQSTA-----SGVEVGLRQVASSVAL-FEMLL	52
Db	46	VPGTASGCGVVGAGSDENNRSSAGERGAAGAAGEVNGTAAVGLVVSAGVGCVFLAAE	105
OY	53	DLTAVGAAMVAATYAKTPALRKY--FVHLCLVDLLAALTLPMLAMISSALFDHALF	110
Db	106	ILMAVAGMLILTVSACNRHLOTVTNYETIVNLAVDLLLSATVLPFS--ATMEVIGFMAF	163
OY	111	GEVACRLTFLFVSYCVSLAITSALINERYVVVHPMKRYEVRMLGLVASVVGWMA	170
Db	164	GRAPCDVMAADVLCCTASILSLCTISVDRYGVGRHSLSKTPSIMERKAATALLMANA	223
OY	171	LAMASVPLVGRVSWEGAPSVPPGCSLOWSHSAYQL-----FVVVFAVLYFLPLLLT	225
Db	224	IVVSGPLLG--WKE--PVPP-----DERFCGITEAGVAYFSSLCISFYLLPMATV	270
OY	226	VVYCGMEFVARAAMQHPRLPTMTWPPRORESLSSRSMYWS-----GAPDTPHR	278
Db	271	VMYCIVVYVAASTYS---LEAGVGRERKGAEEVLRILHRSSSTGTDRGHAMSTKCH	327
OY	279	TFGGG-----KAAYVLLAVGQFLLCWLPRFSFILYVALSAOPTSGOVESV	326
Db	328	TFRSSLSRLRLKFSRKREKAAKTALVVCVFVLCMPPEFFVLPLGLFLPOLKPSGEVFKY	387
OY	327	TWIGFCTSNPFPGCINROI RGLSGKOPVCFK-----PÄ	363
Db	388	FWLGTFCNSCVNPLITPCSSREKRAFLRLKQCCHSRRRRRRLKRAYRGHMLASNGCPR	447
OY	364	P-----EEELRLPSREGSTIENFLOFLQGTGCPSESWSVRPLPSPKQEPAY-D	411
Db	448	PDCAPGLGAAREAPLAPAPE-----ATDTPSAPAEQAQPVVGRKKPEYSFSD	495
OY	412	FRIPQIAEETSEFLQOULTDIIMSDSYLRPAASPRLES	451
Db	496	WRLLGPPRRPPTT---OLRAKVVSSLSOKIRGASPCAEA	530

RESULT 7	
09GJS6	
ID 09GJS6	PRELIMINARY;
AC 09GJS6;	PRT; 405 AA.
DT 01-MAR-2001	(TREMBLREl, 16, Created)
	(TREMBLREl, 16, Last sequence update)

DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
DE BETA 3 ADRENERGIC RECEPTOR.  
GN BAR.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;

KR 117  
 RP SEQUENCE FROM N.A.  
 RA Forrest R.H., Hickford J.G.H.:  
 RT "Polymorphism within the ovine beta 3 adrenergic receptor gene."  
 RL Submitted (Oct-2000) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL: AF314204; AAC31167.1; -  
 DR EMBL: AF314202; AAC31165.1; -  
 DR InterPro: IPR000276; GPCR\_nhoopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G-PROTEIN\_RECCEP-FL\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECCEP-FL\_2; 1.  
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
 SO SEQUENCE 405 AA; 42928 MW; ADD3A2BAF814E75 CMC64;

Query Match	14.3%	Score 330.5;	DB: 6;	Length 405;
Best Local Similarity	23.4%	Pred. No. 7.9e-21;		
Matches 116; Conservative	62;	Mismatches 170;	Indels 47;	Gaps 17;

```

QY  / POSSNNSSTLGRVPTP---GPST---ASSVPEGLDVADESVALEFILLLELDLYAAGNAA 62
Db  3 PMPGONS-LTPWPDITPLAAPTAAAGLPGVPW----AVALAGALLAVALATVAGNLL 57

QY  63 VMAVIAKTPALRKf---VVFHLCVLVDLLAALTLMPLAMLSSSALEFDHALFGEVACRLYLF 120
Db  58 VIVAIARTPRLQTMNPEVSTSLATADLYVGLVPPG---ATLALGIMHPLGTGCELTWS 115

QY  121 LSYCVSLAIIISVAINNEYVYVVHPRKREYRMKLGLVASLYGVWVKALAMASVPLG 180
Db  116 VDLVLCVSIETFLCALADRYLATYNTPLRYGALYTKRRARAVALVWVWVAASVAPLMS 175

QY  181 RVSMEGASVPVPGCSLQMSHAVCQL-----FVVFAVLFLPLLLILVYCSMPFAVA 235
Db  176 K-WMRVGDALDAQRH---SNPRCTGFASNMRYALLSSSVTYRLPLVMLVYAAVFVYA 231

QY  236 ---RVAAMQHGRPLTWMETPR-QKSESLSKSTWVYSSGAP-----QTPHRTFGGG 283
Db  232 TROLRLRLRELGRPFEEESPAPASGSGSPGAPGAPVAPAGVPSYGRDPAALLPREH--- 288

QY  284 KAAVYLLAVGQFLCMLPRTFSFHLVYVLSAQPISTGQVESVYTWIGYFCTSPNFFFGC 343
Db  289 RALRTLIGIMCTFTLCMLPFVVVNVVRAALGSPSLVSGPTFLAAMLGYANSAFNPLIY-C 347

QY  344 LNRQIRGSLSKQFVCFKAPDEEL-----RLPS 372
Db  348 RSPDRSAF-RRLLC--RCPEEHTLAASPPAPPS 379

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RESULT 8		
Q9MZ00		
ID	Q9MZ00	PRELIMINARY;
AC	Q9MZ00;	PRT; 407 AA.
DT	01-OCT-2000 (TREMBLrel. 15, Created)	
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE	BETA-3-ADRENERGIC RECEPTOR.	
OS	Sus scrofa (Pig).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
OX	NCBI_TaxID=9823;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Smith T.R., Bidwell C.A., Mills S.E.;	

RT "Sus scrofa beta-3-adrenergic receptor (BAR3) gene."  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 DR EMBL: AF274007; AAF82301.1; -  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS: PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
 SQ SEQUENCE 407 AA; 43610 MW; C65983829A38DD9 C6C64;

Query Match 14.2%; Score 329; DB 6; Length 407;  
 Best Local Similarity 28.6%; Pred. No. 1.1e-20;  
 Matches 125; Conservative 61; Mismatches 177; Indels 74; Gaps 21;

OY 4 SPIPOSSGNSSTIGRVPQTGPST-----ASGVPEGLRDVASEVALPFMLLD-L 54  
 DB 2 APWPQ--GNSS-----LPPRPDYSTLAPNNANSGLPV-----PMAVALAGALLAPVL 49  
 OY 55 TAVGNAAMAVIAKTPALRKF--VFPHLCVLDLLAALTPLMLSSALFDHALFGE 112  
 DB 50 ATVGGNLLVIAIARTPLQWTNVEVTSLATADLVGLVLPVPG--TTIALTGHMPLGA 107  
 OY 113 VACRLYLELSCFVSLATLSAIVERYYYVHPMYREVRMTGLVASLVGVVAKALA 172  
 DB 108 TCCELMTSYDVLCTASLETGLALAVDRLATVNPRLRGALTKRRARAVALVWVNSA 167  
 OY 173 MASVFLGRVSWEGAPSVPPGCSLOWSHAYCOL-----FVVYFAVLVFLPLLLIV 227  
 DB 168 VSFARIMSK--MWRVGADADAQRCH--SNPSCCTFASNNPVALSSSYFLPLVLMFLV 223  
 OY 228 YCSMFRVARVAMQGRPLTW--METPRORSESLSRSTMTSSGAPOTTPHRTGGGKA 285  
 DB 224 YARVF-----VATSQLRLRLRMELSRFPPEESPAPSRK--QSPAPGRPMSPAGVPSHGRR 278  
 OY 286 AVLL-----AVGGFLLCMLPYEFHLYVALASAPISTGQVESVVTMIGYFC 333  
 DB 279 PARLLPLREHRLCTGLMGFTTLCMLDPFVYVNVVNRALGSPVPAFLALNMGYAN 338  
 OY 334 FTSNPFYGLNROIRGELSKQVCFKPAPEEELRL--PSREGSIEENFLOFLOGTGP 391  
 DB 339 SAFNPLIY-CHSPDRSAF--RRLLC--RCGPPEHLAASPPAPR-----GAP 382  
 OY 392 SESWVRPLSPKQEP 408  
 DB 383 ET--LTHPAES--RQSP 396

RESULT 9  
 O63004 PRELIMINARY; PRT; 438 AA.  
 AC O63004;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE 5-HT6 SEROTONIN RECEPTOR.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN-SPRAGUE-DAWLEY; TISSUE-STRATUM;  
 RA MEDLINE=96102917; PubMed=8522988;  
 RA Kohen R., Metcalf M.A., Khan N., Druck T., Huebner K., Lachowicz J.E.,  
 RA Melzer H.Y., Sibley D.R., Roth B.L., Hamblin M.W.;  
 RT "Cloning, characterization, and chromosomal localization of a human 5-  
 RT HT6 serotonin receptor."  
 RL J. Neurochem. 66:47-56(1996).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

DR EMBL: L41146; AAB92633.1; -  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS: PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
 SQ SEQUENCE 438 AA; 46786 MW; DB90403892F691A9 C6C64;

Query Match 14.2%; Score 328; DB 11; Length 438;  
 Best Local Similarity 27.4%; Pred. No. 1.4e-20;  
 Matches 129; Conservative 61; Mismatches 184; Indels 96; Gaps 19;

OY 2 ESSPIPOSSGNSSTIGRVPQTGPSTASGVPEVGLRDVASEVALPFMLLDLTVAAGNA 61  
 DB 4 EPGPV-----NST--PAMGPGPPAG-----GSGVMAALCVIYVLT-A--ANS 45  
 OY 62 AMAVIAKTPALRKF--VFPHLCVLDLLAALTPLMLSSALFDHALFGEVACRLYL 119  
 DB 46 LLIVICTOPAVRNTSNFFVLSFTSDLMVGLVWPPAML--NALYGRVILARGLCLMT 103  
 OY 120 FLSCFVSLATLSAIVERYYYVHPMYREVRMTGLVASLVGVVAKALMASVPVL 179  
 DB 104 AFDVCCSASITLNCILSIDRLLILSLRYKLRMTAPRALILIGASIALASFLPL 163  
 OY 180 GRVSNME--GAPSV--PGCSLOWSHAYCOL-----FVVYFAVLVFLPLLLIVYCSMF 232  
 DB 164 --LGMHEIKARTPAPG-----OQRLLASLPFLVASGVTFELSGALCFYTCRL 212  
 OY 233 RVARVAMQGRPLTW-----ETPRORSESLSRSTMTSSGAPOTTPHRTGG 281  
 DB 213 LAARKQAVVASLTGTGAQALETLQVPRTPRGMSADSRRLATKHSKAL----- 264  
 OY 282 GKAAVVLNAGGQFLCMLPYEFHLYVALSAQPISTGQVESVVTMIGYFCFTSNPPFY 341  
 DB 265 --KASLTGLILGMFVFWLPEFVANIAQAV--CDCISPLFD-VLTWLGYSNTMNPITY 320  
 OY 342 GCLNQIRGELSKQVCFKPAPEE-----LRLP----- 371  
 DB 321 PLFMDPFRKALGRPLCVHCP--PEHRASPAFSPSMKTSHGARGSLQGVLPSPNSD 379  
 OY 372 SREGSIEENFLOFLOGTGPSESWVRPLSPKQEPADVFRIPQIAEE 421  
 DB 380 SPSASGGTSGQLDTQOLLPGEA--TRDPPPTRTATVYVNFVTSVERE 427

RESULT 10  
 O9GJTO PRELIMINARY; PRT; 405 AA.  
 AC O9GJTO;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE BETA 3 ADRENERGIC RECEPTOR.  
 GN B3AR.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Forrest R.H., Hickford J.G.H.;  
 RT "Ovis aries beta 3 adrenergic receptor (B3AR) gene - allele F,  
 RT complete cds."  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Forrest R.H., Hickford J.G.H.;  
 RT "Polymorphism within the ovine beta 3 adrenergic receptor gene."  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.





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Dh 58 VIVAARTPRLQTMNVEVTSLATADVLGVLPVPG--ATLATGHPMLGVTCGLMTS 115
Oy 121 LSVCFVSLAISVAINERYVYVHPMRVEVMTGLGVASVLGVWKALAMASVPLG 180
Dh 116 VDVLCAVTSITLALAVDRLATVNPRLGALYTKRRARAVALVWVSAVSAPLMS 175
Oy 181 RVSMEGAPSVPCSLQMSHAYCOL-----FVVFVAVLFLPLLLILVYCSMPFVA 235
Dh 176 K-WMRVGAADAQORCH---SNPRCCTFASNMYPALLSSVSFYLPVLMLVYARVYVA 231
Oy 236 ---RVAAHQGLPTWMTETPR-QRSESLSSRSSTWVTSSGAP-----QTPHRTGGG 283
Dh 232 TROLRLRLRELGRPPPEESPAPSRGSPGAPVSPGVSGRRPARLLPLREH--- 288
Oy 284 KAAVVLAVAGQFLCMLPYPFPHLYVALSQPISTGVESVWIGFCTSNPFPGC 343
Dh 289 RALFTLGLIMGTFLCMLPFVVVNVVRALGGPSLVSQPTLALMWLGANSAPNPLAY-C 347
Oy 344 LNRQIRGELSKOFVCFKFAPEEELRLPS 372
Dh 348 RSPDFRSAP-RRLIC--RCPEEHLAAS 373

RESULT 13
O9NG02 PRELIMINARY; PRT; 399 AA.
AC O9NG02
DT 01-OCT-2000 (Tremblrel, 15, Created)
DT 01-OCT-2000 (Tremblrel, 15, last sequence update)
DE 01-DEC-2001 (Tremblrel, 19, last annotation update)
DE G-PROTEIN COUPLED RECEPTOR.
GN TYR1.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Eukaryota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Apis.
OX NCBI_Taxid=7460;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20155587; PubMed=10693920;
RA Blenau W., Ballanz S., Baumann A.;
RT "myt1.1: characterization of a gene from honeybee (Apis mellifera)
RT brain encoding a functional tyramine receptor.";
RL J. Neurochem. 74:900-908(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AJ245824; CAB76374.1; -.
DR HSSP: P29274; 1MMH.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G-PROTEIN_RECEPTOR_FL_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEPTOR_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 399 AA; 44650 MW; F5FE4E4F1336433 CRC64;

Query Match 13.98; Score 322; DB 5; Length 399;
Best Local Similarity 23.68; Pred. No. 4.3e-20;
Matches 100; Conservative 64; Mismatches 139; Indels 88; Gaps 12;
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Dh 188 -----COLTRQGVYIYSSLSQSFIFLLMSLVLEILATRRRLRERARSRINAYOST 242
Oy 242 -----HGRLPTWETPRKRS--LSSRSFMTSSGAPQTPHRTFGG 282
Dh 243 RHRADAESVSSETHNE---RSTPRSHAKPSLIDDEPTEVTIGGGTSSRRRTGS 298
Oy 283 -----GKAAVVLAAAGQFLCMLYFPHLYVALSAQPI 318
Dh 299 RAAATTTVVFIEERORISLSKERRAARLGVIMGVVCMPLPFMLYVLPCCPDCP 358
Oy 319 TGQVESVWTVIGFCTSNPFYGLNQR 349
Dh 359 SDRMYVFTWGLGVNSALNPLITITFNLDYR 389

RESULT 14
O9OX46 PRELIMINARY; PRT; 402 AA.
AC O9OX46
DT 01-DEC-2001 (Tremblrel, 19, Created)
DT 01-DEC-2001 (Tremblrel, 19, last sequence update)
DE 01-DEC-2001 (Tremblrel, 19, last annotation update)
DE SC:B22015.4 (NOVEL PROTEIN SIMILAR TO HUMAN G-PROTEIN COUPLED RECEPTOR RE2).
GN SC:B22015.4.
OS Brachydanio rerio (Zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL590146; CAC94897.1; -.
KW Receptor.
SQ SEQUENCE 402 AA; 44373 MW; 5FB8875874267F00 CRC64;

Query Match 13.78; Score 318.5; DB 13; Length 402;
Best Local Similarity 27.78; Pred. No. 8.8e-20;
Matches 96; Conservative 69; Mismatches 145; Indels 37; Gaps 11;
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DT 01-MAY-2000 (Tremblrel. 13, last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)  
 DE ALPHA 1-ADRENERGIC RECEPTOR SUBTYPE ALPHA 1D, ALPHA 1D-AR.  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 ON NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9210054; PubMed=1661838;  
 RA Perez D.M., Plascik M.T., Graham R.M.;  
 RT "solution-phase library screening for the identification of rare  
 RT clones: isolation of an alpha 1d-adrenergic receptor cDNA.";  
 RL Mol. Pharmacol. 40:876-883(1991).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KM G-protein coupled receptor; Glycoprotein; Transmembrane.  
 SQ SEQUENCE 559 AA; 59739 MM; 37CD9BD696D3A47D CRC64;

Query Match 13.78; Score 316.5; DB 11; Length 559;  
 Best Local Similarity 26.18; Pred. No. 1.9e-19;  
 Matches 102; Conservative 76; Mismatches 156; Indels 57; Gaps 15;

QY 6 IPQSSGNSSTL-----GRVPQT-----PGPSTA---SGVPEVGLRDVASEVAL-FFMLILD 53  
 DB 42 VPGATGGGAAVGTSGGETNSSTGEGAAAGEVNNAAGVGLVSAOGVGVGFLAAFI 101  
 QY 54 LTAAGNAANAANAIAKTPALRKFV--EYFHLCLVDLLAALTMLPLMLSSALFDHALFG 111  
 DB 102 LTAAGNLLVLSVACNRHLQTVNYFIYNLAVADLLLSAVALPFS--ATMEVLGFMAFG 159  
 QY 112 EVACRLYLELVCSEVSLAISVAINERYYYVHPMYEVPMTLGLVASVLCVWAKAL 171  
 DB 160 RTFCDVMAAADVLLCTASISLCTISVDRYGVGRHSLSKYPAIMIERKAAAILALMAVAL 219  
 QY 172 AMAVVPVIGRYSWEGASVSPGCSLQWSHSAAYOL-----FVYFAVLVFLPLLLILV 226  
 DB 220 VASVGPLG---MKE---PVPP-----DERFCGITEEVGAIIPSSVCSFYLLPMAVIV 266  
 QY 227 VYCSMFYVAR--VAMQHGRLPTWMEYTPRORSE--SLSSRSITWYSSGAP--QTPPHRT 279  
 DB 267 MYCAVYVVARSTTSLEAG---IKREPKASEVVLRIHCRGARTSAKGYPGTQSSKQHT 322  
 QY 280 FGGC-----KAAYVLLAVGGOFLLCWLPEYFSLHYVALSAQPISTGOVESVYT 327  
 DB 323 LRSSLVRLLEKFSREKKAAKTLAIYGVFVLCWPEFFFLPLGSIPIKPSGEVFKYIF 382  
 QY 328 WIGYFCFTSNPFYGCINROI RGLSKQFVC 358  
 DB 383 WLGTFNSCVNPLIYPCSSREKRAFLRLRC 413

Search completed: October 21, 2002, 16:10:47  
 Job time : 37 secs